

FIG. 1

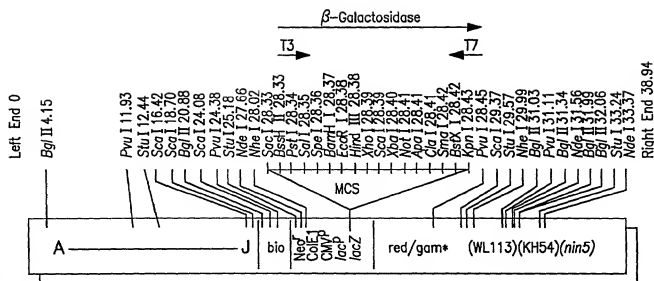


FIG. 2A

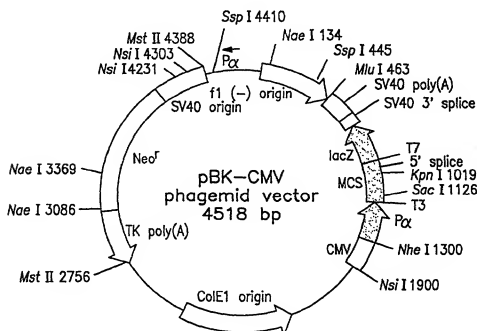


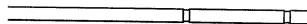
FIG. 2B

QC-RT-PCR primers for the 5' coding sequence of
Candida tropicalis 20336 P450CYP52A5A

5'	ATGATTTGAACAACCTCTAGAAATATTGGTAT	GTGCTTTGTGCCAGTGTGTGACATCATCAAA	CAACTCCTTGCATACACAAGAAGCTCGCGTC	3'	90
3'	TACTAACTTGTTGAGATCTTTATAACCAT	CAGCAACACGGTCACAACATGTAGTAGTTT	GTTGAGGAACGTATGTGTTTCTGAGGCGAG	5'	
5'	TTGATGAAAAAGTTGGGTGCTCCAGTC	ACAAACAAGTTGTACGACAAACGCTTTCGGT	ATCGTCAATGGAATGAAGGCTCTCCAGTTC	3'	180
3'	AACTACTTTTTCACCCACGACGAGTCAG	TGTTTGTTCACATGCTGTTCGAAAGCCA	TAGCAGTTTACCTACCTCCGAGAGGTCAAG	5'	
Forward primer 7501-97F					
5'	AAGATAGAGGGCAGGGCTCAAGAGTACAAAC	GATTACAAGTTTGACCACTCCAGAACCCA	AGCGTGGGCACCTACGTCAGTATCTTTTC	3'	270
3'	TTCTTTCTCCCGTCCCGAGTCTCTCATGTG	CTAATGTTCAAACTTGTGTAGGTTCTTGGGT	TGCAACCCGTGGATCGATCATAGAAAG	5'	
5'	GGCACCAGGATCGTGCACCAAGATCCA	GAGATATCAAAAGCTATTTTGGCAACCCAG	TTTGGTGATTTTCTTTGGGCAAGAGGCAC	3'	360
3'	CCGTGGTCTTACGACACTGGTTTCTAGGT	CTCTTATAGTTTCGATTAACCGTTGGGTC	AAACACATAAAGAACCCGCTCTCCGTG	5'	
5'	ACTCTTTTAAAGCTTTGTAGTGATGGG	ATCTTCACATTGGACGGCAAGCGTGGAG	CACACAGAGCCGATGTTGAGACCACAGTTT	3'	450
3'	TTGAAAAATTCGGAACAATCTACTACGC	TAGAACTGTATACCTTCGGCTCCGACCTTC	GTGTGCTCTCGGTACAACTCTGGTGCAAA	5'	
Reverse primer 7501-97R					
5'	GCCAGAGAACAAAGTTGCTCATGTGACGTG	TTGGAACCAACACTTCCAGTTGTGAGAAG	CATATCTTAAGCAACAAGGGTGAAATCTTT	3'	540
3'	CGGTCTCTTGTTCACACGATCACTGCAGC	AACCTTGGTGTGAAGGTCAACAACCTCTCTC	GTATAAGAATTCGTGTTCCCACTTATGAAA	5'	

FIG. 3

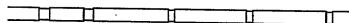
CYP Gene



Helix I

HR2

CPR Gene



FMN-binding
region

FAD-binding
region

NADPH-
binding

FIG. 4

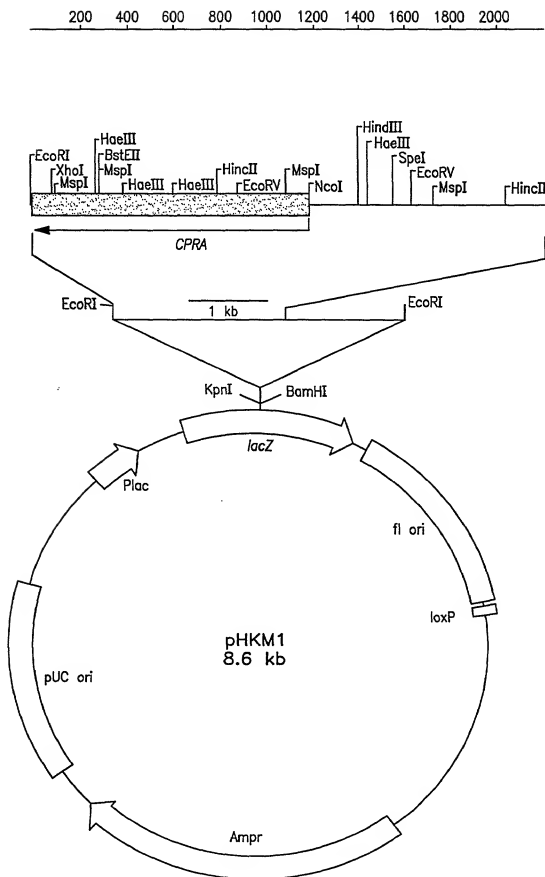


FIG. 5

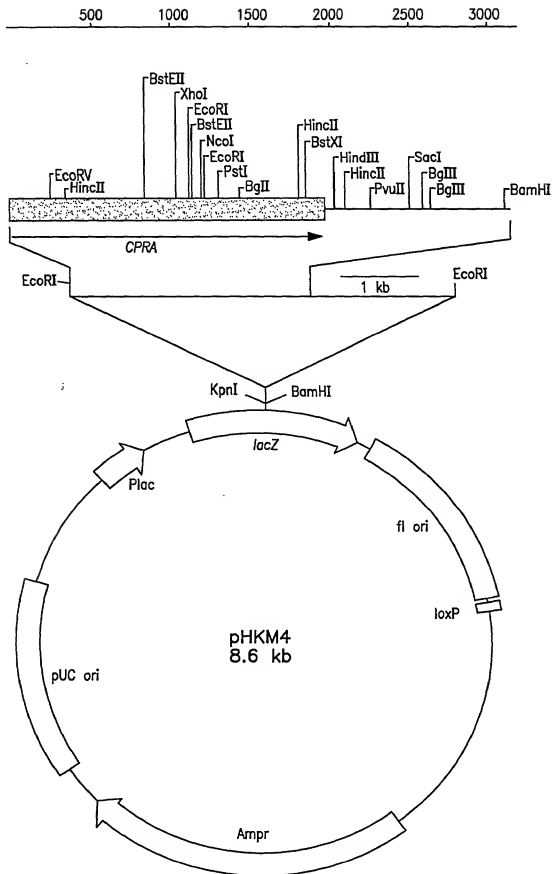


FIG. 6

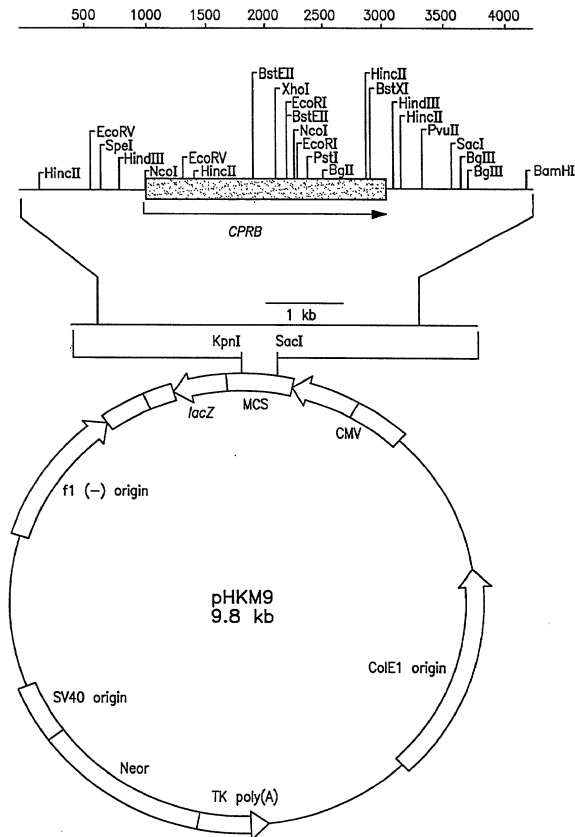


FIG. 7

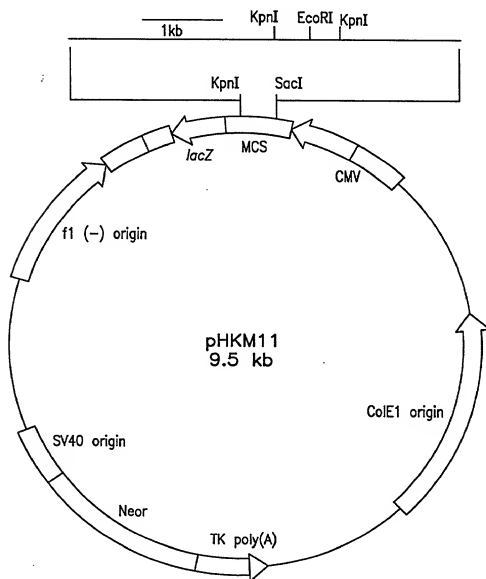
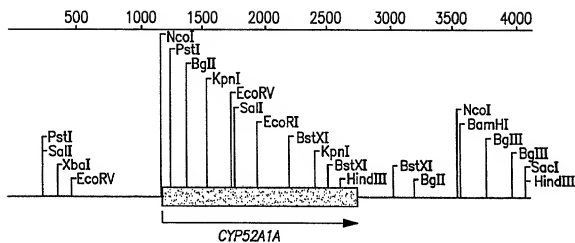


FIG. 8

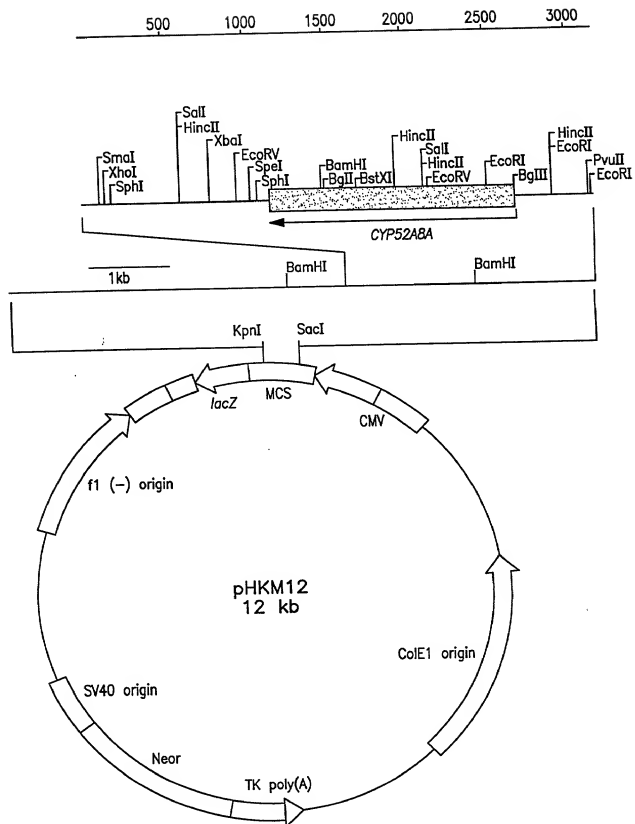


FIG. 9

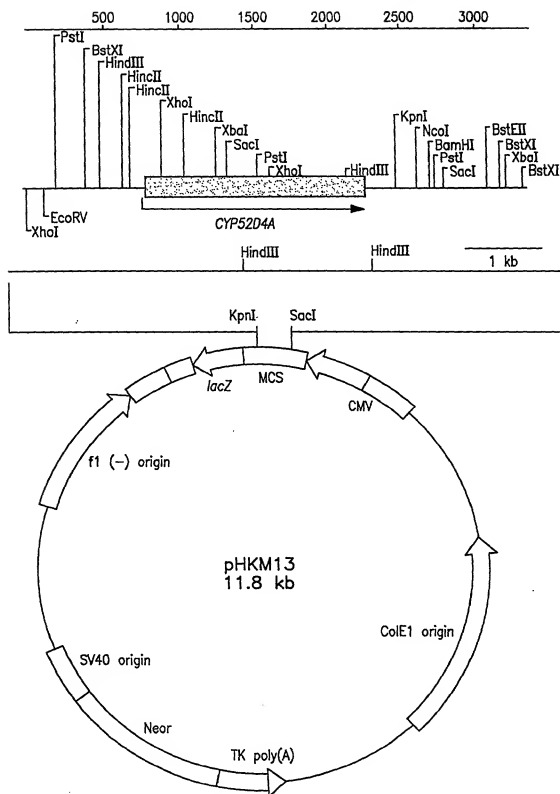


FIG. 10

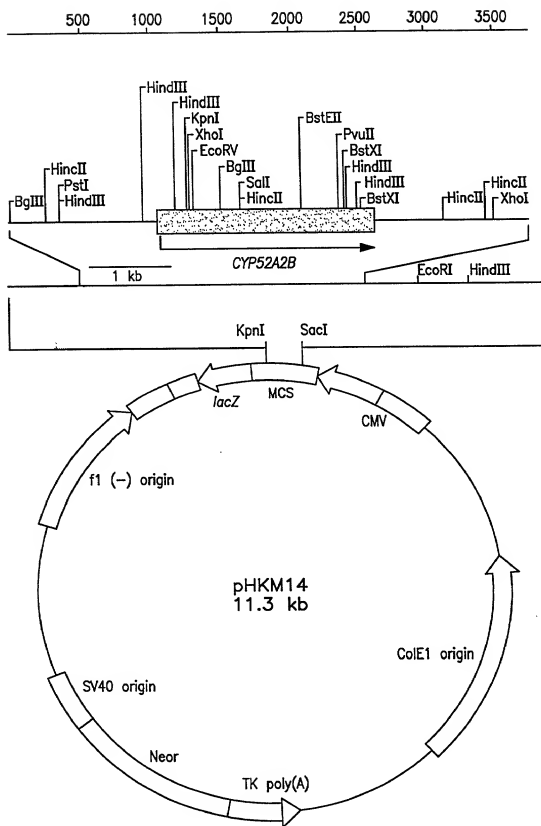


FIG. 11

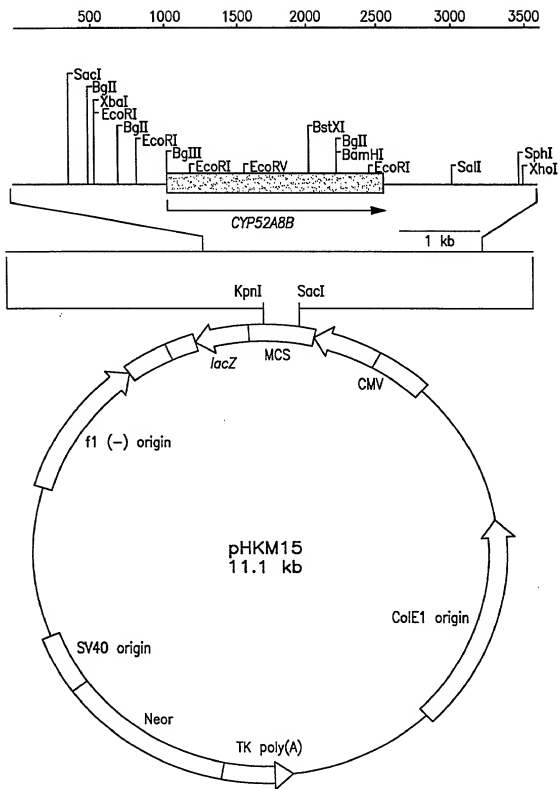


FIG. 12

CPRA	413	CCACCCCTCCCATGAATCAATCAAAAGTTGTGGGGGATCTCCACCAAGGGCAACGGAGTTAAATGCTTATG	488	***** ** *****	552	TTCTCCCACTTTGGTGTGTGATTTGGGTAGTCTAGTCAAGTTGGAGATTTCTTTTTCGCGAGGTCTC	617	TCTTTCCCACTTTGGTGTGTGATTTGGGTAGCTAGTCAAGTTGGTGAATTTCTTTTTCGCGAGGTCTC	622	CGATATCGAAATTTGATGAATATAGAGAGACCCAGATCAGCAACAGTAGATTTGCTTTGTGTAGTAGAT	683	CGATATCGAAGTTTGATGAATATAG --- GAGCCAGATCAGCATGGAATATTTGCTTTGTAGATAGAT	692	GTGGAACGACCAACTAGTTGAATTAACGCCACCACTTTGACAGCAAGTCCAGTGCAGCTGTAACAGATGACG	730	GTTGAAACAACAACCTAGCTGGAATTAACACACACCGCT --- ---- AAACGATGCGC	762	CCAGAGTGTCAACCAACTGACGTTGGGTGGAGTTGTGTGTGTGTGGCAGGGCCATATTGCTTAA	791	ACAGGGTGTCAACCGCAACTGACGTTGGGTGGAGTTG --- ---- TTGTTGGCAGGGCCATATTGCTTAA	832	ACGAAGACAAGTAGCACAAAAACCCAAAGCTTAAGAACAAAAATTAATAAAAAATTCACGACAAATCCAAAG	858	ACGAAGAGNAGTAGCACAAAAACCCAAAGTTTAAGAACAA --- TTAATAAAAAATTCATACGACAAATCCACAG	899	CCATGTGATTACATAT --- CAACAG - TAAGACAGAAAAAATTTTCAACATTTCAAAAGTTCCCTTTTCT	928	CCATTTTACATAATCAACGACGACAAATGAGACAGAAAAAATTTTCAACATTTCAAAAGTTCCCTTTTCT
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FIG. 13A-2

[illegible]

FIG. 13A-3

CPR	1033	GTCAATATAAATTGGTGGTCTGTAGCCGCTTATTTTGTCTAAGAACCAAGTTCCTTGATCAGCCCCAGG	1102
CPRB	1060	GTCAATATAAATTGGTGGTCTGTAGCCGCTTATTTTGTCTAAGAACCAAGTTCCTTGATCAGCCCCAGG	1129
		*****	*****
CPR	1103	ACACCGGTTCTCAACACGGACACGGGAAGCAACTCCAGAGACGCTCTGCTGACATTGAAGAAGATAA	1172
CPRB	1130	ACACCGGTTCTCAACACGGACACGGGAAGCAACTCCAGAGACGCTCTGCTGACATTGAAGAAGATAA	1199
		*****	*****
CPR	1173	TAAAAACACGTTGTTGTTGGTCCAGACCGGTACGGCAGAGAATTACGCCAACAAATTGTCAGA	1242
CPRB	1200	TAAAAACACGTTGTTGTTGGTCCAGACCGGTACGGCAGAGAATTACGCCAACAAATTGTCAGA	1269
		*****	*****
CPR	1243	GAATTGCACTCCAGATTGGCTTGAAACAGATGGTTGCAGATTTCGCTGATTACGATTGGGATAACTTCG	1312
CPRB	1270	GAATTGCACTCCAGATTGGCTTGAAACAGATGGTTGCAGATTTCGCTGATTACGATTGGGATAACTTCG	1339
		*****	*****
CPR	1313	GAGATATCACCGAAGACATCTTGGTGTGTTTCAITGTTGCCACCTATGGTGAAGGTGAACCTACCGATAA	1382
CPRB	1340	GAGATATCACCGAAGATATCTTGGTGTGTTTCAITGTTGCCACCTATGGTGAAGGTGAACCTACCGATAA	1409
		*****	*****
CPR	1383	TGCCGACGAGTTCCAACCTGGTTGACTGAAGAAGCTGACACTTTGAGTACCTTGAATACACCGTGTC	1452
CPRB	1410	TGCCGACGAGTTCCAACCTGGTTGACTGAAGAAGCTGACACTTTGAGTACCTTGAATACACCGTGTC	1479
		*****	*****
CPR	1453	GGGTTGGTGAATCCACGTAACGATTTCTCAATGCAATTGGTAGAAGTTTGACAGATTGTTGAGCGAGA	1522
CPRB	1480	GGGTTGGTGAATCCACGTAACGATTTCTCAATGCAATTGGTAGAAGTTTGACAGATTGTTGAGCGAGA	1549
		*****	*****

FIG. 13B-I

CPRA	1523	AAGTGGTGACAGGTTTGCTGAATA	CGCTGAAGGTGATGACGGTCTCGCA	CCTTGGACGAAGATTTCAT	1592
CPRB	1550	AAGTGGTGACAGATTGCTGAATAT	GCTGAAGGTGACGCGCACTTGGCA	CCTTGGACGAAGATTTCAT	1619
		*****	*****	*****	
		*****	*****	*****	
CPRA	1593	GGCTCGAAGGACAATGTCTTGACGC	CTTGAGAAATGAATGAATGAACCTTT	GAAAGGAATTGAAGTAC	1662
CPRB	1620	GGCTCGAAGGATAATGTCTTGACGC	CTTGAGAAATGAATGAATGAACCTTT	GAAAGGAATTGAAGTAC	1689
		*****	*****	*****	
		*****	*****	*****	
CPRA	1663	GAACCAACGTTGAATTGACTGAGAG	GACGACTTGTCTGTCTGTGACTCCCA	AGTTTCTTGGGTGAGC	1732
CPRB	1690	GAACCAACGTTGAATTGACTGAGAG	GACGACTTGTCTGTCTGTGACTCCCA	AGTTTCTTGGGTGAGC	1759
		*****	*****	*****	
		*****	*****	*****	
CPRA	1733	CAAAACAAGAGTACATCAATCAACT	CCGAGGCGATCGACTTGAACCAAGG	TCCATTCGACCACCCACCCATA	1802
CPRB	1760	CAAAACAAGAGTACATCAATCAACT	CCGAGGCGATCGACTTGAACCAAGG	TCCATTCGACCACCCACCCATA	1829
		*****	*****	*****	
		*****	*****	*****	
CPRA	1803	CTTGGCCAGNAATCACCGAGACGAG	AGATTGTTTCACTCCAAGGACAGAC	ACTGTATCCAGCTTGAATTT	1872
CPRB	1830	CTTGGCCAGGATCACCGAGACGAG	AGATTGTTTCACTCCAAGGACAGAC	ACTGTATTCACGTTGAATTT	1899
		*****	*****	*****	
		*****	*****	*****	
CPRA	1873	GACATTTCTGAATCGAACTTGAAAT	ACACCCGGTGACATCTAGCTATCT	GGCCATCCAACTCCGAGC	1942
CPRB	1900	GACATTTCTGAATCGAACTTGAAAT	ACACCCGGTGACATCTAGCTATCT	GGCCATCCAACTCCGAGC	1969
		*****	*****	*****	
		*****	*****	*****	
CPRA	1943	AAACATTAAGCAATTGGCAAGTGT	TTCCGATTGGAAGATAAACTCGAC	ACTGTTATGTAATTGAAGGC	2012
CPRB	1970	AAACATTAAGCAATTGGCAAGTGT	TTCCGATTGGAAGATAAACTCGAC	ACTGTTATGTAATTGAAGGC	2038
		*****	*****	*****	
		*****	*****	*****	

FIG. 13B-2

CPRA CPRB	2013 2040	GTTGACTCCACTTACACCATCCCAATCCCAACCCCAATACCTACGGTCTGTCAATTAGACACCATTTA ATTGACTCCGACTTACACCATTCCAATCCCAACTCCCAATTAACCTACGGTCTGTCAATTAGACACCATTTA *****	2082 2109
CPRA CPRB	2083 2110	GAAATCTCCGGTCCAGTCTCGAGACAATCTTTTGTCAATTGCTGGGTTGCTCTGTGATGAAGAACA GAAATCTCCGGTCCAGTCTCGAGACAATCTTTTGTCAATTGCTGGGTTGCTCTGTGATGAAGAACA *****	2152 2179
CPRA CPRB	2153 2180	AGAAGGCTTTTACAGACTTGGTGTGACAAAGCAAGATTCCCGCCCAAGTCAACCCGCAAGAAAGTTCAA AGAAGACTTTTACAGACTTGGTGTGACAAACAGAAATTCGCCACCAAGTTACCCGCAAGAAAGTTCAA *****	2222 2249

FIG. 13B-3

CPR	2223	CATTGCCGATGCGCTTGTTATATTCCTCCAAACACGCTCATTGGTCCGATGTTCTCTTTGAATTCCTTATT	2292
CPRB	2250	CATTGCCGATGCGCTTGTTATATTCCTCCAAACACATCCATGGTCCGATGTTCTCTTTGAGTTCTTATT	2319
		*****	*****
CPR	2293	GAAACGTTCCACACTTGACTCCACGTTACTACTCATTTCTGTTCTTCGTTCAATGAGTGAAGAACACTCA	2362
CPRB	2320	GAAACATCCAAACACTTTGACTCCACGTTACTACTCATTTCTTCGTTGAGTCAAAAACACTCA	2389
		***** * *	*****
CPR	2363	TCAACGTTACTGACAGTTGTTGAAGCGCAAGAGAGCTGATGGCAGACCACTCACTGCTGTTGTACCCAA	2432
CPRB	2390	TCAATGTTACTGACAGTCGTTGAGGCGAAGAGAGCGGATGGCAGACCACTCACTGCTGTTGTACCCAA	2459
		*** ***** *	*****
CPR	2433	CTTGTTGAAGAACGTTGARAATTGTGCMAAACAAAGACTGGCGAAAAGCCACTTGTCCTACTACGATTTGAGC	2502
CPRB	2460	CTTGTTGAAGAACATTTGAATAATTGGCAAAACAAAGACTGGCGAAAAGCCACTTGTTCTACTACGATTTGAGC	2529
		*****	*****
CPR	2503	GGCCCAAGAGGCAAGTTCAACAAGTTGCAGTTGCCAGTGCATGTGAGAGAATCCAACTTTAAGTTGCCAA	2572
CPRB	2530	GGCCCAAGAGGCAAGTTCAACAAGTTGCAGTTGCCAGTGCACGTGAGAGAATCCAACTTTAAGTTGCCAA	2599
		*****	*****
CPR	2573	AGAACTCCACACCCACAGTTATCTTGATTGGTCCAGGTACTGGTGTTCGCCCATTGACAGGTTTGTCTAG	2642
CPRB	2600	AGAACTCCACACCCACAGTTATCTTGATTGGTCCAGGTACTGGTGTTCGCCCATTGACAGGTTTGTCTAG	2669
		*****	*****
CPR	2643	AGAAAGAGTTCAACAAGTCAAGAAATGGTGTCAATGTGGCAAGACTTTGTTGTTTATGGTTGCAGAAC	2712
CPRB	2670	AGAAAGAGTTCAACAAGTCAAGAAATGGTGTCAATGTGGCAAGACTTTGTTGTTTATGGTTGCAGAAC	2739
		*****	*****

FIG. 13C-I

CPRA	2713	TCCAACGAGACTTTTGTACAAAGCAAGAAATGGCGGAGTACGCTTCGTGTTGGTGAAACTTTGAGA	2782
CPRB	2740	TCCACGAGGACTTTTGTACAAAGCAAGAAATGGCGGAGTACGCTTCGTGTTGGTGAAACTTTGAGA	2809

CPRA	2783	TGTTCAATGCCCTCTCCAGACAAGACCCATCCAAGAAGGTTTACGTCAGGATAGATTTTAGAAAAACAG	2852
CPRB	2810	TGTTCAATGCCCTCTCTAGACAAGACCCATCCAAGAAGGTTTACGTCAGGATAGATTTTAGAAAAACAG	2879

CPRA	2853	CCAACTTGTGACGAGTTGTGACTGAAGGTGCCATTATCTACGTCCTGTGTGATGCGCAGTAGAATGGCT	2922
CPRB	2880	CCAACTTGTGACGAGTTGTGACTGAAGGTGCCATTATCTACGTCCTGTGTGATGCGCAGTAGAATGGCC	2949

CPRA	2923	AGAGAGCTCGACACCAACATTTCCAAAGATTGTTGCTAAAGCAGAGAATTAGTCAAGACAAGGCTGCTG	2992
CPRB	2950	AGAGAGCTCGACACCAACATTTCCAAAGATTGTTGCTAAAGCAGAGAATCAGTGAAGACAAGGCCGCTG	3019

CPRA	2993	AATTGGTCAAGTCTCGGAAGTCCAAAATAGATACCAAGAAGATGTTTGGTAGACTCAACGAATCTCTC	3062
CPRB	3020	AATTGGTCAAGTCTCGGAAGTCCAAAATAGATACCAAGAAGATGTTTGGTAGACTCAACGAATCTCTC	3089

CPRA	3063	TTTCTCCCAACGCATTTATGAATCTTTATCTTCATTTGAAGCTTTACATATGTTCTACACTTTATTTTTT	3132
CPRB	3090	TTTCTCCCAACGCATTTATGAATCTTTATCTTCATTTGAAGCTTTACATATGTTCTATATTTCAITTTTT	3155

CPRA	3133	TTTTTTTTTTTATTTATATTACGAACATAGTCAACTATATATACTTTGATTAATGTTATAGAAACAA	3202
CPRB	3156	TTT-----ATTATATTACGAACATAGTCAACTATATATACTTTGATTAATGTTATAGAAACAA	3215

FIG. 13C-2

CPRA	3203	TAACTATTATCTACTCGTCTACTTCTTTGGCAATTGACATCAACATTACCGTTCCATTACCGTTGCCGTT	3272
CPRB	3216	TAAATTATTATCTACTCGTCTACTTCTTTGGCAATTGGCAATTGGCAATTGGCAATTGGCAATTGGCGTT	3285
		*** *****	*** **
		*** *****	*** **
CPRA	3273	GGCAATGCCGGGATATTTAGTACAGTATCTCCAATCCGGATTTCAGCTATTGTAGATCAGCTGCAAGTCA	3342
CPRB	3286	GGTAATGCCGGGATATTTAGTACAGTATCTCCAATCCGGATTTCAGCTATTGTAAATCAGCTGCAAGTCA	3355
		** *****	*****
CPRA	3343	TTCTCCACCTTCAACCCAGTACTTATACCTTCATCTTTGACITTCAGTCCAGTCAATAATATTACAAGTTA	3414
CPRB	3356	TTCTCCACCTTCAACCCAGTACTTATACCTTCATCTTTGACITTCAGTCCAGTCAATAATATTACAAGTTA	3425
		*****	*****

FIG. 13C-3

CPRA CPRB	3413 3426	GCAAGAACTTCTGGCCATCCACGATATAGACGTTATTACAGTTATTATGCGAGTATGATGGTTATC GCAAGAACTTCTGGCCATCCACATATAGACGTTATTACAGTTATTATGCGAGTATGATGGTTATC *****	3482 3495
		CTTATTGAACTTCTCAAACCTTCAAACACCCACGTCCTCCGCAACGTCATTATCAACGACAAGTTCTGG CTTATTGAACTTCTCAAACCTTCAAACACCCACGTCCTCCGCAACGTCATTATCAACGACAAGTTCTGA *****	3552 3565
CPRA CPRB	3553 3566	CTCAGTCGTGGAGCTCGTCAAAGTTCTCAATTAGATCGTTCCTGTTATTGATCTTCTGTAATTCTCA CTCAGTCGTGGAGCTCGTCAAAGTTCTCAATTAGATCGTTCCTGTTATTGATCTTCTGTAATTCTCA *****	3622 3635
		ATTCTGGAACACATTGTCCTCGTTGTTCAAATAGATCTTGAACAACCTTTTCAACGGGATCAACTTCTC ACTGCTGGAACACATTGTCCTCGTTGTTCAAATAGATCTTGAACAACCTTTTCAAGGGAATCAACTTTC *****	3692 3705
CPRA CPRB	3693 3706	AATCTGGCCAAAGATCTCCGCGGATCTTCAGAAACAAGTCTGCAACCCCTGGTCGATGGTCTCGGG GATCTGGCCAAAGATCTCCGCGGATCTTCAGAAACAAGTCTGCAACCCCTGGTCGATGGTCTCGGG *****	3762 3775
		TACAACAAGTCCAAGGGCGAAGATGTTAGGCAAGTGTTCAACTGGTTCAACGACATGTTTCGACAGT TACAACAAGTCTAAGGGCGAAGATGTTAGGCAAGTGTTCAACTGGTTCAACGACATGTTTCGACAGT *****	3832 3845
CPRA CPRB	3833 3846	AGTTGAGTTATGTTATCGTACAAACATTTGTTGTTGATTTCGAAATGACGAGCTGATGCCATCAT AGTTGAGTTATGTTATCGTACAAACATTTGTTGTTGATTTCGAAATGACGAGCTGATGCCATCAT *****	3902 3915

FIG. 13D-1

CPRB	3903	CTCTGGTTCCTTCATAGTACAACTGGCACTTCTTCGAGAGGCTCAATTCTCGTAGTTCCTCCGTCGAAG	3972
CPRB	3916	CTCCTGGTTCCTTTCATAGTACAACTGGCACTTCTTCGAGAGACTCAACTCCTCGTAGTTCCTCCGTCGAAG	3985
		*****	*****
CPRB	3973	ATATTGGCAACAAGAGCCCGTACCGCTCACGAGCATCAAGTCTGTGGCCCTGGTTGTTCAACTTGTGTA	4042
CPRB	3986	ATATTGGCAACAAGAGCCCGTAGCGCTCACGAGCATCAAGTCTGTGGCCCTGGTTGTTCAACTTGTGTA	4055
		*****	*****
CPRB	4043	TGAAGTCCGAGCTCAAGACAATCAACTGGATGTCGATGATCTGGTGGGGAACAAGTTCCTTGCATTTTAG	4112
CPRB	4056	TGAAGTCCGATGTCAGACAATCAACTGGATGTCGATGATCTGGTGGGGAACAAGTTCCTTGCATTTTAG	4125
		*****	*****
CPRB	4113	CTCGATGGAAGTCGTACAACTCACAGTCGAGATATACTCCTGTTCTCTTCAAGAGCCGGATCCGCAAG	4182
CPRB	4126	CTCGATGAAGTCGTACAACT	4125

CPRB	4183	AGCTTGTGCTTCAAGTAGTCGTTG	4206
CPRB	4146		4145

FIG. 13D-2

CPRB	60	MALDKLDLYVITLWVA	VAAYFAKNQFLDQPDGTGFLNTDGGNSRDVLLTLKKNKNTL
CPRB	60	MALDKLDLYVITLWVA	VAAYFAKNQFLDQPDGTGFLNTDGGNSRDVLLTLKKNKNTL
CPRB	120	LLFGSQTGTAEDYANKLSRELHSRFG	LTKWADFADYDNDNFGDITEDILVFFIVATYGE
CPRB	120	LLFGSQTGTAEDYANKLSRELHSRFG	LTKWADFADYDNDNFGDITEDILVFFIVATYGE
CPRB	180	GEFTDNADFEHTWLTEADTL	STLKYTVFGLGNSTYEFFNAIGRKFDRLISEKGGDRFAE
CPRB	180	GEFTDNADFEHTWLTEADTL	STLKYTVFGLGNSTYEFFNAIGRKFDRLISEKGGDRFAE
CPRB	240	YABGDDGTGTLDEDFMAWKDNVFDAL	KNDLNPEEKELKYEPNVKLTERDDLSAADSQVSL
CPRB	240	YABGDDGTGTLDEDFMAWKDNVFDAL	KNDLNPEEKELKYEPNVKLTERDDLSAADSQVSL
CPRB	300	GEPNKKYINSEGIDLTKGPFDPHTHPYLARI	TETRELFSKDRHCIHVEFDISESNLKYTT
CPRB	300	GEPNKKYINSEGIDLTKGPFDPHTHPYLARI	TETRELFSKDRHCIHVEFDISESNLKYTT
CPRB	360	GDHLAIWPSNSDENIKQFAKCFGLEDKLD	TVIELKALDSTYTPFPPTITYGAVIRHHLE
CPRB	360	GDHLAIWPSNSDENIKQFAKCFGLEDKLD	TVIELKALDSTYTPFPPTITYGAVIRHHLE
CPRB	420	ISGPVSRQFFLSIAGFAPDEETKKAFT	RLGGDKQEFATKVTTRKFNADALLYSSNNA PW
CPRB	420	ISGPVSRQFFLSIAGFAPDEETKKAFT	RLGGDKQEFATKVTTRKFNADALLYSSNNTPW
CPRB	480	SDVPPEFLIENVPHTTPRYSISSSLSSEKOL	INVTAVVEAEAEADGRPVTGVVTNLLKN
CPRB	480	SDVPPEFLIENVPHTTPRYSISSSLSSEKOL	INVTAVVEAEAEADGRPVTGVVTNLLKN

FIG. 14A

	* *		
CPRA	VEIQNTGKPLVHYDLSGPRGKFNKFLPVHRRSNFKLPKNSTTPVILIGPGTGVP	540	
CPRB	IEIAQNTGKPLVHYDLSGPRGKFNKFLPVHRRSNFKLPKNSTTPVILIGPGTGVP	540	
CPRA	LRGFVRERVQOVKNGVNVGKTLIFYGCRNSNEDFLYKQEWAEYASVLGENFEMFNFSRQ	600	
CPRB	LRGFVRERVQOVKNGVNVGKTLIFYGCRNSNEDFLYKQEWAEYASVLGENFEMFNFSRQ	600	
CPRA	DPSKKVYVQDKILENSQLVHELLTEGAI IYVCGDASRMARDVOTTISKIVAKSREISEDK	660	
CPRB	DPSKKVYVQDKILENSQLVHELLTEGAI IYVCGDASRMARDVOTTISKIVAKSREISEDK	660	
CPRA	AAELVKSWKVQNRVQEDVW	680	
CPRB	AAELVKSWKVQNRVQEDVW	680	

FIG. 14B

CYP52A1A	1	GACCTGTGACGCTTCCGGTGTCTTGGCCACAGTCTCCAAAGTTGACCGAGCGCCCAAGTCAATGTACCACTTT	70
CYP52A2A	1		0
CYP52A2B	1		0
CYP52A3A	1	GACATCATAT	11
CYP52A3B	1		0
CYP52A5A	1		0
CYP52A5B	1	TTACAATCATGG	12
CYP52A8A	1		0
CYP52A8B	1		0
CYP52D4A	1		0
CYP52A1A	1	CATATGGCGTAACTCTCTTCTTTTCTTTTATATCAAGGAGAAACTATCCCACCCCCACTTC	59
CYP52A2A	71	ATTTCCGGTTACACTTCCAAGATGGCTGTACTGAAGAAGGTTCACGGAACCAACCAAGCTACTTCTCCG	140
CYP52A2B	1		0
CYP52A3A	12	GACCCGGTTAATTCGCCCTCAGGTTGCTTATTGAGCCGTAAAGTCAGTAGAAACTTTGCCITGGGGTTC	81
CYP52A3B	1		0
CYP52A5A	1	TTGAGTC	7
CYP52A5B	13	AGCTCGTAGGAACCCAGATGTCTGGGAGAAGCTCCGCGAAGAGGTCAACACGNACTTTGGCATGGAGTC	82
CYP52A8A	1		0
CYP52A8B	1		0
CYP52D4A	1		0

FIG. 15A-1

CYP52A1A	60	GAACACAAATGACAACTCCTCGGTAACTTGCAAAATCTTGCTGCACTAAATGAAAACTCCGGACGAGTCA	129
CYP52A2A	141	CTTGTTCGGTCAACCATTCCTTGGTGTGCAACCAATGAAGTACGCTCAACAATTCCTGACAAAGATCTC	210
CYP52A2B	1	GCTCAACAATTTGCTGACAAAGATCTC	26
CYP52A3A	82	AAACTCTAGTATAAATGSGTGATAACTGGTTGGCACCTCTTGCCTAGGCATGAAAATAGGCCGTTATAGTACT	151
CYP52A3B	1		0
CYP52A5A	8	GCCAGACTTGCTCACTTTTGTACTCCCTTCGAAACTCAAAGTACGTTCAAGCGGTGCTCAACGAAACGCTC	77
CYP52A5B	83	GCCAGACTTGCTCACTTTTGTACTCTTTAGAAAGCTCAAGTACGTTCAAGCGGTGCTCAACGAAACGCTT	152
CYP52A8A	1		0
CYP52A8B	1	AAAACCGATACAAGAAAGACAGTCAA	28
CYP52D4A	1		0
CYP52A1A	130	GACCTCCAGTCAAAACGACACAGACAGACAAACAACCTTGGTGGCATGTTCACTACCTACAGACATGTCAACGGG	199
CYP52A2A	211	GCAACACAAAGGCTAACGCTTGGTTGTAACACACCGGTTGGGTGGTCTTCTGCTGCTAGAGGTGGTAAG	280
CYP52A2B	27	GCAACACAAAGGCTAACGCTTGGTTGTAACACACCTGGTTGGGTGGTCTTCTGCTGCTAGAGGTGGTAAG	96
CYP52A3A	152	ATAATTTAAATGAAGCTAGGAGTATAGGATGCATATGACCGGTTTTTCTATATTTTTTAAGATAATCTCTAGT	221
CYP52A3B	1	CCTGCGAGA	8
CYP52A5A	78	CGTATCTACCCCGGGGTACCAACGAAACATGAAGACAG--CTACGTTGCAACACGAGTTGCCACGCGGAGG	145
CYP52A5B	153	CGTATCTACCCCGGGGTGCCACGAAACATGAAGACAG--CTACGTTGCAACACGAGCTTCCCGCGTGGAGG	220
CYP52A8A	1		0
CYP52A8B	29	CAGAAACGTTAAATGTCACACCGCGGCCCAAGAGACAGG--TTTGGCGGACTTGGAAAGAAATGTGGCATTTGC	96
CYP52D4A	1		0

FIG. 15A-2

CYP52A1A	200	TGTTAGACACGGTTTCTTGC AAAAGAC - AGGTGTTGGCATCTCGTACGATGGCACTGCAGGAGGTGTCTG	268
CYP52A2A	281	AGATGCTCATTTGAAGTACACCAAGAGCCATTTTGGACGCTATCCACTCTGGTGAATTTGCCAAGGTTGAAT	350
CYP52A2B	97	AGATGTTTCATTTGAAGTACACCAAGAGCCATTTTGGACGCTATCCACTCTGGTGAATTTGCCAAGGTTGAAT	166
CYP52A3A	222	AAATTTTGTATTTCTAGTAGATTTTCATCAAAATTCGCAACCAATTTCTGGCGAAAAAATGATCTTTTAC	291
CYP52A3B	9	ATTCCGCGCCGCTCGACAGATGACGATTTGCAAGCATGTGATTTGTGTTTTCGCAACCTGTTTGCCAC	78
CYP52A5A	146	AGGCA - AAGACGCGCAAGGAACCTATCT - TGGTGCAGAAGGACAGTCCCGTTGGGTTGATTAATTTGCCA	213
CYP52A5B	221	AGGCA - AAGACGCTAAGGAACCTATTT - TGGTGCAGAAGGCGCAGTCCCGTTGGGTTGATTAATTTGCCA	288
CYP52A8A	1	CCATG - ATGTTTATGTTCTGGAGAGGT - TTTTCAAGGAATCGTCACTCTCCGCCACCAAGAACCA	0
CYP52A8B	97		164
CYP52D4A	1		0

FIG. 15A-3

CYP52A1A	269	ACTTCTCTTTAGGCAATAGAAAGACTTAAGACAGACAGCGTTTTTACAGTTGCATTTGGTTAATGTAGT	338
CYP52A2A	351	ACGAAACTTTCCAGTCTTCAACTTGAATGTCCCAACCTCTCGTCCAGGTGTCCCAAGTGAATCTTGAA	420
CYP52A2B	167	ACGAGACTTTCCAGTCTTCAACTTGAATGTCCCAACCTCTCGTCCAGGTGTCCCAAGTGAATCTTGAA	236
CYP52A3A	292	GTCAAAAGCTGA-ATAGTGCAGTTTAAAGCACCTTAAATACATAACAGCCCTTAGATACGACAGAGAA	360
CYP52A3B	79	GACAAATGATCG-ACAGT-CGATT--ACGTATCCCATATTTATTTAGAGGGGTAAATAAAATTAATGGCA	144
CYP52A5A	214	CGCAGACGGACCCAGAGTATTTTGGGGCGAGCTGTGGTGTGAGTTTAAAGCCGGAGAGATGTTTGTATCA--	281
CYP52A5B	289	CGCAGACGGACCCAGAGTATTTTGGGGCGAGTGTGGTGTGAGTTTCAAAACCGGAGAGATGTTTGTATCA--	356
CYP52A8A	1	GTTAACGAGATCCATATTTCAAAACCCAGGAGTGAATGCTCAACAAACACAGCAACAAACA--	0
CYP52A8B	165	GTTAACGAGATCCATATTTCAAAACCCAGGAGTGAATGCTCAACAAACACAGCAACAAACA--	232
CYP52D4A	1	GTTAACGAGATCCATATTTCAAAACCCAGGAGTGAATGCTCAACAAACACAGCAACAAACA--	0
CYP52A1A	339	ATTTTCTTTAGTCCAGCATTTCTGTGGTGTGCTCTGGGTTTCTAGAAATAGAAATCAAGAGAAATGCAAA	408
CYP52A2A	421	CCCAACCAAGCCCTGGACCGG-AAGGTGTTGACTCTCTTCAACAAAGAAATCAAGTCTTTGGCTGTAAGT	489
CYP52A2B	237	CCCAACCAAGCCCTGGACCGG--AAGGTGTTGACTCTCTTCAACAAAGAAATCAAGTCTTTGGCTGTAAGT	304
CYP52A3A	361	GCTCTTTATGATCTGAAGAAGCATTTAGAAATGCT---ACTATGAGGCACCTATTGGTGTATATATTAGGGA	427
CYP52A3B	145	GCC----AGAAATTTCAACATTTTGCAACAACATGCAAAATGAGAACTCCACAGAGAAATAAATAA	210
CYP52A5A	282	AGCATGAAGAACTTGGGGTGTAAATACTTGGCTTCAATGCTGGGCCACGGACTTGTCTGGGGCAGCAGT	351
CYP52A5B	357	AGCATGAAGAACTTGGGGTGTAAATACTTGGCTTCAATGCTGGGCCACGGACTTGTCTGGGGCAGCAGT	426
CYP52A8A	1	AGCATGAAGAACTTGGGGTGTAAATACTTGGCTTCAATGCTGGGCCACGGACTTGTCTGGGGCAGCAGT	0
CYP52A8B	233	ACCCCAACAGAAACAGTGGAAATAATGCCAGTCAA-CAAAAGAGTGGTGAACAGACGAGGGAGAAACGCAAG	301
CYP52D4A	1	ACCCCAACAGAAACAGTGGAAATAATGCCAGTCAA-CAAAAGAGTGGTGAACAGACGAGGGAGAAACGCAAG	0

FIG. 15B-I

CYP52A1A	409	TT	CAGATGGAAGAA	CA	AGAGAT	AAAA	CAAAAA	AAAAA	AAAT	CGAT	TTTT	TG	CCAA	TAA	GA	TGTT	---	474		
CYP52A2A	490	TT	CGTGA	AAAC	--	TT	CAAG	CC	TAT	GT	CG	CAAG	TA	CT	AC	CG	CTGA	--	555	
CYP52A2B	305	TT	GT	CTGA	AAAC	--	TT	CAAG	CC	TAT	GT	CG	CAAG	TA	CT	AC	CG	CTGA	--	370
CYP52A3A	428	TT	GGT	GCA	TT	AA	GT	AC	GT	CT	TA	TAA	CA	GA	AA	TA	CT	TA	AA	497
CYP52A3B	211	AC	TC	CG	CA	CC	AA	CA	AA	CA	AA	CA	AA	CA	AA	CA	AA	CA	AA	267
CYP52A5A	352	AC	ACT	TT	CA	TT	GA	AG	CG	AG	CT	AT	TT	GT	AG	TC	CG	GT	TT	416
CYP52A5B	427	AC	ACT	TT	CA	TT	GA	AG	CG	AG	CT	AT	TT	GT	AG	TC	CG	GT	TT	491
CYP52A8A	1	CA	AC	TT	GT	GA	TT	GT	AG	TC	CG	GT	TT	GT	AG	TC	CG	GT	TT	0
CYP52A8B	302	CA	AC	AG	T	GG	T	GG	T	GG	T	GG	T	GG	T	GG	T	GG	T	366
CYP52D4A	1	GA	T	GT	GG	T	GG	T	GG	T	GG	T	GG	T	GG	T	GG	T	GG	58
CYP52A1A	475	-	AT	GA	T	CA	T	CA	CC	AT	CG	T	CA	A	A	A	A	A	A	543
CYP52A2A	556	CT	TA	AG	AT	TA	TT	AT	TA	TT	AG	TT	GG	CT	AT	TT	CT	CA	T	624
CYP52A2B	371	CT	TA	AG	AT	TA	TT	AT	TA	TT	AG	TT	GG	CT	AT	TT	CT	CA	T	439
CYP52A3A	498	-	TA	GG	AG	CC	TT	TT	CT	GA	CA	TT	CG	GT	CG	CA	CC	AT	C	556
CYP52A3B	268	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	329	
CYP52A5A	417	-	CG	CC	AG	TA	CG	GG	GT	TAC	-	CA	CC	AA	GA	AG	AT	CG	T	484
CYP52A5B	492	-	CT	GC	AG	GG	T	CG	GG	T	AC	-	CA	CC	AA	GA	AG	AT	CG	559
CYP52A8A	1	-	CA	TA	T	GG	CC	AT	CA	TA	T	GG	CC	AT	CA	TA	T	GG	CC	0
CYP52A8B	367	-	CA	TA	T	GG	CC	AT	CA	TA	T	GG	CC	AT	CA	TA	T	GG	CC	435
CYP52A4A	59	-	TC	GT	TA	AG	CA	CA	GG	AA	CT	GT	CT	CA	CA	CT	TA	T	GC	127

FIG. 15B-2

CYP52A1A	544	ACATGAAGTGAATCCAAA-TACACTACACTCGGGTATTGCTTCCTTGTGTTTACAGATGTCCTCATTGTC	612
CYP52A2A	625	ATATAAAGTTACTTCGGA-----TATCAATTGTAATCGTGCCTGTCGCAATGGATGATTTGGAA	683
CYP52A2B	440	ATATAAAGTTATTTGGGAAC-TCATA--TATCAATTGTAATCGTGCCTGTTGCAATGGGTAAATTTGAAA	505
CYP52A3A	567	AATAATAGTGAACCTTTGTG-TAATAAATCTTCTGCAAGACTTGCATAAATTCGAGCTTGGGAGTTCAACG	635
CYP52A3B	330	GATGTGTTGGTTTCTACAA-TGCAAGGGCACAGTTGAAGGTTTCCACATAACGT-TGCACCATATCAAC	397
CYP52A5A	485	TGT--AAAGCTTTATAAGGA-TGTAACGGTAGATGGATAGTTGTGTAGGAGGAGCGGAGATAAAATTAGAT	551
CYP52A5B	560	TGT--AAAGTTTCAAGGA-TCTAGATGGATATGTA-AGGTGTGTAGGAGGAGCGGAGATAAAATTAGAT	625
CYP52A8A	1		0
CYP52A8B	436	CCA--ATAAGACTATCCCTT-CTTACAACCAAGTTTCTGCCGGCCCTGTCTGGCA-ACAGATGCTGGCC	501
CYP52D4A	128	GATATCTGCCAAGGTATATAGCAGAAGCTGCTGATGTTCTCTCGGTCAATATCTGTGTGTTAGTTCTTGCA	197

FIG. 15B-3

CYP52A1A	613	TTACTTTTGAGTCTATAGGAGTTGCTGTGTGAGAGATCACAGATTAATCACTCACATTTATCGTAGTT	682
CYP52A2A	684	CTGGCGTTGAAACCGAATTCATGACGACGCGGAGA-TAAAGAATPACGT-----AATTTATCTCTTGAGACA	749
CYP52A2B	506	CTGTAGTTGGAAACCGAATTCATGACGATCGGAGA-TAACACG-----AGATTATCTCTTAAGACA	565
CYP52A3A	636	C--CAATTTGACCTCGTTTCATGTGATAAAGAAAGCCAAAGGTAATT---AGCAGACGC---AATGGG	697
CYP52A3B	398	T--CAATTTATCTCAATCATGTGTGATAAAGAGAGCCAAAGGTAATT---GGCAGACCCCCCAAGGG	462
CYP52A5A	552	TTGATTTTG---TGTAAAGTTTGGATGTCAACCTACTCCGCACTTCATGCA-GTGTGTGTGACACAAGG	617
CYP52A5B	626	TTGATTTTG---TGTAAGTTTAGCACACGCTACTCCGCACTTTGT-----GTGTAGGAGGACACA---	685
CYP52A8A	1		0
CYP52A8B	502	GACACACTT---TCAACTGAGTTTGGTCTAGAAATTTCTTGCACTGACGACA-AGGAAACTCTTACAAAG	567
CYP52D4A	198	GGTAAATTTGGATGTCACAGTAGTGGAGGAGGTTTGATCGGTTGTGT-TTCTTTCTCTCTCTCTCTGT	266
CYP52A1A	683	TCCTATCTCATGCTGTGTCTCTGTTTGGTTCATGAGTTTGGATT---GTTGTACATTAAAGGAATCGCT	750
CYP52A2A	750	ATTTTAGCCGTGTTACACGCCCTTCTTTGTT-CTGAGGGAAGGAT--AAATAATTAGACTTCCACAGCT	816
CYP52A2B	566	ATTTTGGCCTCATTCACGCCCTTCTT---CTGAGCTAAGGAT--AAATAATTAGACTTCCACAGTT	628
CYP52A3A	698	AACATGGAGTGGAAAGCAATGGAACACGCC--AGGACGAGTAATTTAGTCCACATACATCTGCGGGT	766
CYP52A3B	463	AACATGGAGTAGAAGCAATGGAACACGCC--ATGACAGTCCCATTTAGCCCCACACATCTAGTATT	531
CYP52A5A	618	GTGTACGTGTGTCGTGTCGCGCCACAGACA--GCCCAAGGGG--TGTGTAGTGT-GTGTGTGGCGGNA	681
CYP52A5B	686	---TACTCCGCTCTGCGCTGTGCCAAGAGACG---GCCACGGG-----TAGTGT-GTGTGTGGTGAA	741
CYP52A8A	1	GAATTCCTTTGGATCTAATTCACGCTGATC---TTGCTAATCCT--TATCAAAGTATTGATGATCAT	62
CYP52A8B	568	--ACACACACTGTGCTCTGATGCCACTTGATC---TTGCTAAGCCT--TATCAAAGTATTGATGATCAT	630
CYP52D4A	267	ATTCAACCTCCACGCTCTCCTTCGCGTTTCTGTGTGTGATC--GTACTGTGTGATTAAAGTCCATC	334

FIG. 15C-I

CYP52A1A	751	GGAAAGCAAGCTAACTAAATTTTCTTTGTCAAGGTACACTAACCTGTAAAACTTCACTGCCACGCCAG	820
CYP52A2A	817	CATTCTAATTTCCGT----CAGCGGAATATTGAA-----GGGGGTTACATGTGGCCGCTGAA-	869
CYP52A2B	629	CATTAAATATCCGT----CAGCGAARACTGCAACAATAAGGAAGGGGGGTAGACGTAGCGGATGAA-	694
CYP52A3A	767	-----TTTTTTTTTGTGGCGCAAGTACACACCTGGACT--TTAGTTTATGGCCCCATAAAAGTTTAAACAATCTAA-	830
CYP52A3B	532	CTTTTTTTTTTGTGGCGAGTGCACACCTGGACT--TTAGTTTATGGCCCCATAAAAGTTTAAACAATCTCA-	599
CYP52A5A	682	GTGCATGTGACACA---ACGGTGTGGTCTGGCCAAATGGTGGATAAGTGCAGGTAAGCAGCGACCTGAA	748
CYP52A5B	742	GTGCATGTGACACA---ATACCCTGGTTCTGGCCAAATGGGGGATTTAGTGTAGGTAAGCTGCGACCTGAA	808
CYP52A8A	63	GTTTGTCTGAATTTAT--ACACACCAAGTGGAAAGATATGGTCTTAATTTGCACGCTCCCATGGCAATTGTG--	128
CYP52A8B	631	GTTTGTCTGAATTTAT--ACACACCAAGTGGAAAGATATGGTCTTAATTTGCACGCTCATGGGCATTGTG--	696
CYP52D4A	335	GCAATGTGAAAAAAGTAGCGCTTATTTACACAACCAAGTTCGTTGGGGGGGTATACAGAAATAGTCTGTT	404
CYP52A1A	821	TCTTTCTGTATTGGCAAGTGCACAAACTACA-ACCTGCAAAACAG-----CACTCCGCTTGTCAAGGTT	885
CYP52A2A	870	-TGTGGGG--CAGTAAACGCAGTCTCTC-----CTCTCCCAAGGAATAGTGCACACGG	918
CYP52ACB	695	-TGTGGGTGGCCAGTAAACGCAGTCTCTCTCTCCCGCCCCCCCCCCCCCTCAGGAATAGTACACCG	763
CYP52A3A	831	-CCTTTGGC-TCCTCAACTCTCTCCGCCCAATATTCGTTTT--ACACCTCAAGCTAGCGACAGCAC	897
CYP52A3B	600	-CCTTTGGC-TCCTCCAGTGTCTCCGCCCTCAGATGCTCGTTTT--ACACCTCGAGCTAACGACACAC	665
CYP52A5A	749	ACATTCCTCAACGCTTAAAGACACTGTTGGGTAGAGATCGGGCCAGGA---CTATTCTTGTCTGT--GCTA	811
CYP52A5B	809	ACATCTCTAACGCTTGAGACACTGTTGGGTAGAGATCGGGCCAGGA---GGCTATTCTTGTCTGT--GCTA	875
CYP52A8A	129	-TGTTT-----GTGGGGGGGGGGGTGACACATTTTGTAGTGCCA---TTCCTTGTGTGATTAC-CCCT	187
CYP52A8B	697	-TGTTT--GGGGGGGGGGGGGTGACACATTTTGTAGTGGAAATGTTTGTGTGCTGTTCC-CCCT	762
CYP52D4A	405	GTGCACGACCATGATATGCAACTTTGACGACGCTGTTAGGA-----ATCCACAGAAATGATGACGAA	469

FIG. 15C-2

CYP52A1A	886	GTCTCCTCTCAACCAACAAAATAAGATTAAACTTTCTTTGCTCATGCATCAATCGGAGTTATCTCTG	955
CYP52A2A	919	AGGAAGGATAACGGATAGAAAGCGGAATGCGAGGAAAT--TTTGAACGCGCAAGAAAGCAATATCCGG	986
CYP52A2B	764	GGGAAGGATAACGGATAGCAAGTGGAAATGCGAGGAAAT--TTTGAATGCGCAAGAAAGCAATATCCGG	831
CYP52A3A	898	AACACCCATTAGAGGAATGGGCAAAGTTAAACACTTTTGGCTTCAATGAATTCCTATTCTACTACATT	967
CYP52A3B	666	AACACCCATTAGAGGAATGGGCAAAGTTAAACACTTTTGGCTTCAATGAATTCCTATTCTACTACATT	729
CYP52A5A	812	CCCGCGCATGGGA-AAATCAACTCGGGGAAGAA--TAAATTTATCCGTAGAAATCCACAGAGCG-----G	872
CYP52A5B	876	CCCG-TGCACGGA-AAATCGAATTCAGGGAAGAA--CAAATTTATCCGTAGAAATCCACAGAGCG-----G	935
CYP52A8A	188	CCCCCTATCAT----TCATTTCCACAGGATTAG--TTTTTTTCTCTCACTGGAAATTCGCTGTCC-----	244
CYP52A8B	763	CCCCCTCCCCCTATCATGCCACAGGATTAG--TTTTTTTCTCTCACTGGAAATTCGCTGTCC-----	822
CYP52D4A	470	GCTTACTACGTGAGAGATCTGCTTAGAGGATG--TTCTCTCTCTTGTGTGATTCATTTAGGTGGGTATCAT	537

FIG. 15C-3

CYP52A1a	956	A--AAGAGTTGCCTTTTGTTGTAATGTTGTCGCAAA-CTCAAACTGC AAAAATAACACACGAATGAT----	1011
CYP52A2a	987	GCTACACAGTTTGGAGCCAGGGAACACACTCTTATTTCTGCTCAATCAACTCAACTGACATAGAAAAA----	1050
CYP52A2b	832	GCTATCAGGTTTGGAGCCAGGGAACACACTCT--CTTCTGCGA AAAA ACTTAACGTGACGAAAAA AAAA	900
CYP52A3a	968	CTTCTCTGTTTGTGCTTTGAATTGCACCATGTGTAATAAAGCAAAATATATATACCTTTTTCATC----	1034
CYP52A3b	730	--CTCTGTGTTTGTGTTTGAATTGACCATGTGAATAAAGCAAAATATATATACCTTTTCGTCTC----	793
CYP52A5a	873	A--TAAATTTGCCACTCTCCATCATCAACACAG--CCGCCATCTACATCATCTCCCTCATTTT----	933
CYP52A5b	936	A--TAAATTTGTCAATGCTGCGTTGCGCAC-----ACACAGCATCTCTC-----	978
CYP52A5b	936	-----ACCTGTCAACCGCCCGCCCGCCCGCC--CCACTGCC--CTACCTTGCCCTCTGC-----	293
CYP52A8a	245	-----ACCTGTCAACCGCCCTCAG-----TGCCCTGCCCCTGC-----	853
CYP52A8b	823	CTCCGGTGGTGACAACTTGAACAAGCAGTTCCGAGAAACCAACCAACAATCATCACTTCCAGC-----	601
CYP52D4a	538		
*			
CYP52A1a	1017	TTCCCTCAAAATATATAAATGACCAACACCATTTCCACACAGCCGTAAATTTCAATGCTCAC-TTTCTCTTTT	1085
CYP52A2a	1051	-----CACAAACGGAATGAACCGCACATGGACAATTAGACCTCCCACTATGATGTTGCTTTAAAC	1115
CYP52A2b	901	AACTCCACGACACAAATGAATCGCACATGGACATTTAGACCTCCCACTATGTAAGAAAGCTTCTCTGGCG	970
CYP52A3a	1035	CTCTCTCATATCTCTTTTGTCTAC-AATTTTGTGTTTTCAGTTTCTTGCTTTTGCACTCTCCCACTCCC	1103
CYP52A3b	794	TGTCCTCAATGCTCTTTTGTCTGCCAATTTTGCTTTTGTGCTTTTGTGTTTGTGCACTCTCTCCCACTCCC	863
CYP52A5a	934	CTCTCTCTCTTTGCTTTATCTCCGCTCCGTTTCTTATCCAGAAATACACACCACTCATATAAAGAT	1002
CYP52A5b	979	CTCGACGCTCGTGTGTTTGTGCTGTGTTTCCACAGCTATAAAGCCCTTGCGCTACGCGCAAGGTTTT	1048
CYP52A8a	294	CTCGACGCCCTGTGTTTGTGCTGTGCTCATCCACAGCTATATACACCACTATGTTTCTTGGCAATCTCTATTGTT	363
CYP52A8b	854	TATCACTTCTACATGCTCAACTAGATGATCTCATCAACCACTAGTTTCTTGGCAATCTCTATTGTT	923
CYP52D4a	602		671

FIG. 15D-2

* *

CYP52A1A	1224	ATGGTACACTGTGATTACTGCAGCAGTATTAGTCTTCTTATCTCCAAACATCAAGAACTACGTC	1293
CYP52A2A	1237	ATGGTACGTGATAGTACCACCTCGCTTGGATTGCTTATAGAGTCTCGACTACTTCTATGCGAGATACTTG	1306
CYP52A2B	1110	ATGGTACGTGATAGTACCACCTCGCTTGGATTGCTTATAGAGTCTCGACTACTTCTATGCGAGATACTTG	1179
CYP52A3A	1209	ATGGTACTACTTCAATACCTTTGGTGGCTCTTTGGTTGAACCTTATAAGTTTGCTCCACACAAAGTACTTG	1278
CYP52A3B	996	ATGGTACTACTTCAATCCCTTTGGTGGCTCTTTGGTTGAACCTTCAATCAGCTTGCTCCACACAAAGTACTTG	1065
CYP52A5A	1128	--GGTATGTGCTTGTGCCAGTGTGTACATCATCAACAACTCTTGGCTACAGCAAGACTCGCGTCTTG	1195
CYP52A5B	1167	--GGTATATGTGTGCGCTGTGTGTACATCATCAACAACTCTTGGCTACAGCAAGACTCGCGTCTTG	1234
CYP52A8A	489	--GGTACATTGTCTTGCCATTGTGGCCATTATCAACAGATCGTGGCTCATGTCAGGACCAATTATTTG	556
CYP52A8B	1042	--GGTACATTGTCTTGCCATTGTGGCTCATATCAAGCAGATCGTGGCTCATGTCAGGACCAATTATTTG	1109
CYP52D4A	798	-TGATCTGTGTCGCTCTTCATTGGCGTTTGGTGTATTTCGGGTAT-GAATATTGTTATAATAACTACTTG	865

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FIG. 15D-3

CYP52A1A	1294	GCAAGAATAATTGAAATGTGTGATCCACCACTACTGAAAGATGCCGTCTCATCTGGTATTCTGCTCTTGA	1363
CYP52A2A	1307	ATGTACAAGCTTGGTGTAAACCAATTTTCCAGAAACAGACAGACGGCTGTTTCGGATTCAAAGCTCCGC	1376
CYP52A2B	1180	ATGTACAAGCTTGGTGTAAACCAATTTTCCAGAAACAAACAGACGGTATTTCGGATTCAAAGCTCCAC	1249
CYP52A3A	1279	GAAACGAGTTTCCAGCGCAAGCCACTCGGTAACTTTGTACGGGACCCCTACGTTTGGTATCGCTACTCCGT	1348
CYP52A3B	1066	GAAACGAGTTTCCAGCGCAAGCCACTCGGTAACTTTGTACGGGACCCCTACGTTTGGTATCGCTACTCCGT	1135
CYP52A5A	1196	ATGAAAAGTTGGGTGCTGCTCCAGTCAAAACAAAGTTGTACGACAAACGCTTTTCGGTATCGTCAATGGAT	1265
CYP52A5B	1235	ATGAAAAGTTGGGTGCTGCTCCAGTCAAAACAAAGTTGTACGACAAACGCTTTTCGGTATCGTCAATGGAT	1304
CYP52A8A	557	ATGAAAGAAATTTGGGTGCTTAAGCCATTACACACGCTCCAACTGACGAGGGTGGTGGGCTTCAAATTCGGCC	626
CYP52A8B	1110	ATGAAAGAAATTTGGGTGCTTAAGCCATTACACATGTCCAACCTAGACGGGTGGTGGGCTTCAAATTCGGCC	1179
CYP52D4A	866	ATGCACAAACATGGCGCTCGAGAAATTCAGAAATGTGATCAACGATGGGTTCCTTTGGGTTCGGCTTACCTT	935
		* * *	
CYP52A1A	1364	TCCGCCCATCAAGGCCCAAGAACGACGGTAG-ATTGGCTAACTTTGCC-----GATGAAGTTT-----	1421
CYP52A2A	1377	TTGAATTGTTGAAGAAGAGAGCGACGGTAC-CCTCATAGACTTTCACA-----CTCAGCGTATC---C	1436
CYP52A2B	1250	TTGAATTGTTTAAAGAAAGAGTGACGGTAC-CCTCATAGACTTTCACHT-----CTCAGCGTATC---C	1309
CYP52A3A	1349	TCGTTTGTATCTACTTGAAGTCGAAAGGTAC-GGTCAATGAAGTTTGGCTGGGGCTCTGGAAACAAAGT	1417
CYP52A3B	1136	TGATCTTGATCTACTTAAAGTCGAAAGGTAC-AGTCATGAAGTTTGGCTGGAGCTTCTGGAAACAAAGT	1204
CYP52A5A	1266	GGAAGGCTCTCCAGTTCAAGAAAGAGGGCAGGCTCAAGAGTACAACG-----ATTACAAGTTTG----	1325
CYP52A5B	1305	GGAAGGCTCTCCAGTTCAAGAAAGAGGGCAGGCTCAAGAGTACAACG-----ATTACAAGTTTG----	1364
CYP52A8A	627	GTGAATTCCTCAAGCAAAAGTGCTGGAG-CTTGGTTGATTTAATC-----ATCTCCCGTTT-----	684
CYP52A8B	1180	GTGAATTCCTCAAGCAAAAGTGCTGGAG-CTTGGTTGATTTAATC-----ATCTCCCGTTT-----	1237
CYP52D4A	936	TGCTACTCATGCGACCAATGAGGGCG-ACATTATCGAGTTTCAGT-----GTCAAGAGATTCGAGT	998
		* * *	

FIG. 15E-1

CYP52A1A	1422	----	CGAGAGTACCCAAACACACCTTCTACTTGTCTGTTGCGGTGCTTTGAAGATTGTCATCACTGT	1487
CYP52A2A	1437	ACGATCTCGATCGTCCGATATCCCAACTTTTACATTTCCCAATCTTTTCCATCAACCTTGTCAATACCTT	1506	
CYP52A2B	1310	AAGGCTCAATCGTCCAGATATCCCACTTTTACATTTCCCAATCTTTTCCATCAACCTTATCAGACACCT	1379	
CYP52A3A	1418	ACATGTCAGAGACCCAAAGTACAAGACCACTGGGCTCAGGATGTTGGCTCCCATTTGATTGAACCAT	1487	
CYP52A3B	1205	ACATTTCAAAGACCCAAAGTACAAGACCACTGGCCTTAGAATTTGTGGCTCCCATTTGATTGAACCAT	1274	
CYP52A5A	1326	ACCACTCAAGAACCCNAGCGTGGGCACCTACGTCAAGTATTTCTTTTGGCACCAAGATCGTGTGACCAA	1395	
CYP52A5B	1365	ACAGTCCAAAGAACCCNAGCGTGGGCACCTATGTCAAGTATTTCTTTTGGCACCAAGATTTGTGTGACCAA	1434	
CYP52A8A	685	-----CCACGA-----TAATGAGGACACTTTCTCCAGCTATGTTTGGCAACCATGTGGTGTTCACAG	744	
CYP52A8B	1238	-----CCACGA-----TAATGAGGACACTTTCTCCAGCTATGTTTGGCAACCATGTGGTGTTCACAG	1297	
CYP52D4A	999	CGGGCCACAT--CCACAGAACAGACATTTGGTCAACCGGCAATGAGCGTTCTCTGTGATACTACCAA	1065	
		*		**
CYP52A1A	1488	TGACCCAGAAAACATCAAGGCTGTCTTGGCCACCCCAATTCACCTGACTTCTCTTGGGTACCAAGACGCG	1557	
CYP52A2A	1507	TGAGCCGGAGAACATCAAGGCAATCTTGGCCACTCAGTTCAAAGATTTCTCTTGGGTACCAAGACCTCG	1576	
CYP52A2B	1380	TGAGCCGGAGAACATCAAGGCTATCTTGGCCACCCAGTTTCAAGGATTTCTCTTGGGCAACAGACACTCG	1449	
CYP52A3A	1488	GGACCCAGAACATCAAGGCTGTTTGGCTACTCAGTTCAAAGATTTCTCTTGGGAACTAGACACGAT	1557	
CYP52A3B	1275	AGACCCAGAGAACATCAAGGCTGTGGTGTCTCAGTTCAACGATTTCTCTTGGGAACTAGACAGAT	1344	
CYP52A5A	1396	AGATCCAGAAATATCAAAGTATTTTGGCAACCCAGTTTGGTGAATTTCTTTTGGGCAAGAGGCACT	1465	
CYP52A5B	1435	GGATCCAGAAATATCAAAGGCTTTTGGCAACCCAGTTTGGGCAATTTTCTTTTGGGCAAGAGGCACT	1504	
CYP52A8A	745	GGACCCAGAAATATCAAGGCGCTTTTGGCAACCCAGTTTGGTGAATTTTCTATTGGGCAAGAGGTC	814	
CYP52A8B	1298	GGACCCAGAAATATCAAGGCGCTTTTGGCAACCCAGTTTGGTGAATTTTCTATTGGGAAACGAGGTC	1367	
CYP52D4A	1066	GGACCCAGTGAAATATCAAGGCGATCTATGACCCAGTTTGAAGCTTTTCTCCCTTGGGTGAGACTAC	1135	
			*	**

FIG. 15E-2

CYP52A1A	1558	CACCTTTGCTCTTTGTTGGTGACGGGATCTCTCACTTTGGACGGAGAGGTTGGNAGCACTCCAGAGCTA	1627
CYP52A1A	1559	CACCTTTGCTCTTTGTTGGTGATGGATCTCTTACCTTTGGATGGCGCGCTGGGAAGCACAGAGATCTA	1646
CYP52A2B	1450	CACCTTTGCTCTTTGTTGGGCGATGGTATCTTTTACCTTTGGACGGTGGCGGCTGGNAGCACAGCAGCTA	1519
CYP52A3A	1558	TTCTTGACTCTCTTTGTTGGTGACGGTATTTTTCACTTTGGACGGTGTGGCTGGGAAACATAGTAGAACTA	1627
CYP52A3B	1345	TTCTTGACTCTCTTTGTTGGGCGATGGTATTTTTTACCTTTGGACGGTGTGGCTGGGCGGAAACACAGTAGAACTA	1414
CYP52A5A	1466	CTTTTAAAACCTTTGTTAGTGATGGATGGGATCTTCAATTTGGACGGAGGCTGGGAGCACAGCAGGCCA	1535
CYP52A5B	1505	CTTTTAAAACCTTTGTTAGTGATGGGATCTTCACTTTGGACGGCGAAGGCTGGNAGCATAGCAGATCCA	1574
CYP52A8A	815	TTCTTCAAAACCATTTATTTGGGTACGGTATCTTCACTTTGGACGGCGAAGGCTGGNAGCACAGCAGAGCCA	884
CYP52A8B	1368	TTCTTCAAAACCATTTGTTGGGTACGGTATCTTCACTTTGGACGGCGAAGGCTGGNAGCACAGCAGAGCCA	1437
CYP52D4A	1136	CAGTGTTCGCGCGTGTGTGGGGAAGGCGATCTTTACTTTTGGACGGCCGACGGTGGNAGCAGCCGACCTA	1205

CYP52A1A	1628	TGTTGAGACCACAGTTTGCTAGAGACCAAGATTGGACACAGTTAAAGCCTTGGAAACCACACATCCAAATCAT	1697
CYP52A2A	1647	TGTTGAGACCACAGTTTGCCAGAGAACAGATTTCACAGTCAAGTTGTTGGAGCCACACAGTTCAGGTGTT	1716
CYP52A2B	1520	TGTTGAGACCACAGTTTGCCAGAGAACAGATTTCACAGTCAAGTTGTTGGAGCCACACATGACAGGTGTT	1589
CYP52A3A	1628	TGTTGAGACCACAGTTTGCTAGAGAACAGAGTTTCCACGTCGAAGTTGTTGGAGCCACACAGTTCAGGTGTT	1697
CYP52A3B	1415	TGTTGAGACCACAGTTTGCTAGAGAACAGAGTTTCCACGTCGAAGTTGTTGGAGCCACACAGTTCAGGTGTT	1484
CYP52A5A	1536	TGTTGAGACCACAGTTTGCCAGAGAACCAAGTTGCTCATGTGACGTGTTGGAAACCACACTTCCAGTTGTT	1605
CYP52A5B	1575	TGTTGAGACCACAGTTTGCCAGAGAACCAAGTTGCTCATGTGACGTGTTGGAAACCACACTTCCAGTTGTT	1644
CYP52A8A	885	TGTTGAGACCACAGTTTGCCAGAGAACAGTTGCTCATGTGACGTGTTGGAAACCACACTTCCAGTTGTT	954
CYP52A8B	1438	TGTTGAGACCACAGTTTGCCAGAGAACAGTTGCTCATGTGACGTGTTGGAAACCACACTTCCAGTTGTT	1507
CYP52D4A	1206	TGTTGCGTCCGCAATTTGCCAAAGATCGGGTTTCTCATATCCTTGGATCTAGAAACCGCAATTTTGTGTTGCT	1275
		**** * ** ** ***** * **** * ** ** * ** ** ** * ** ** *	
CYP52A1A	1698	GGCTAAGCAGATCAAGTTGAACCGGNAAGACTTTCGATATCCAGAAATGTGTTCTTTAGATTTACCGTC	1767
CYP52A2A	1717	CTTCAACACAGTCAAGAAAGGCACAGGCCAAGACTTTTGACATCCAGGAATGTGTTTTCAGATTACCGTC	1786
CYP52A2B	1590	CTTCAAGCAGTCAAGAAAGGCACAGGCCAAGACTTTTGACATCCAGGAATGTGTTTTCAGATTACCGTC	1659
CYP52A3A	1698	CTTCAAGCAGTCAAGAAAGGCACAGGCCAAGACTTTTGACATCCAGGAATGTGTTTTCAGATTACCGTC	1767
CYP52A3B	1485	CTTCAAGCAGTCAAGAAAGGCACAGGCCAAGACTTTTGACATCCAGGAATGTGTTTTCAGATTACCGTC	1554
CYP52A5A	1606	GAAGAAGCATATCTTTAAGCAACAAGGGTGAATACTTTTGATATCCAGGAATGTGTTCTTTAGATTACCGTC	1675
CYP52A5B	1645	GAAGAAGCATATCTTTAAGCAACAAGGGTGAATACTTTTGATATCCAGGAATGTGTTCTTTAGATTACCGTC	1714
CYP52A8A	955	GAAGAAGCATATCTTTAAGCAACAAGGGTGAATACTTTTGATATCCAGGAATGTGTTCTTTAGATTACCGTC	1024
CYP52A8B	1508	GAAGAAGCATATCTTTAAGCAACAAGGGTGAATACTTTTGATATCCAGGAATGTGTTCTTTAGATTACCGTC	1577
CYP52D4A	1276	TCGGAAGCACAATTGATGGCCACAATGAGAGACTACTTCGACATCCAGGAGCTCTTACTTCCGGTTCTCGATG	1345
		** ** * *	

FIG. 15F-I

CYP52A1A	1768	GACACGGCTACTGAGTCTCTTGTGTTGGTGAATCCGTTTCACCTCTGTACGATGAAAAATTGGGCATCCCAA	1837
CYP52A2A	1787	GACTCCGCCACCGAGTTTTTGTGTTGGTGAATCCGTTGAGTCCCTTGAGAGATGAATCTATCGGCATGTCCA	1856
CYP52A2B	1660	GACTCCGCCACTGAGTTTTTGTGTTGGTGAATCCGTTGAGTCCCTTGAGAGATGAATCTATTTGGGATGTCCA	1729
CYP52A3A	1768	GACTCCGCCACCGAGTTCTTGTGTTGGTGAAGTCTGCTGAACTCTTGAGGGACGAATCTATTGGATGTACCC	1837
CYP52A3B	1555	GACTCCGCCACCGAGTCTTGTGTTGGTGAAGTCTGCTGAACTCTTGAGGGACGAATCTATTGGTATCAACC	1624
CYP52A5A	1676	GATTCCGCCACCGAGTTCTTATTGTTGAGTCCGTCGTCGAATCCTTTGAGAGACGACTCTGTGTTGGTTGACCC	1745
CYP52A5B	1715	GACTCCGCCACCGAGTTCTTATTGTTGAGTCCGTCGTCGAATCCTTTAAAGGACGAATCTATGGTATCAACC	1784
CYP52A8A	1025	GACTCCGCCACCGAGTTCTTATTGTTGAGTCCGTCGTCGAATCCTTTAAAGGACGAGAAATTGGCTACGACA	1094
CYP52A8B	1578	GATTGAGCGACCGAGTTCTTATTGTTGAGTCCGTCGTCGAATCCTTTAAAGGACGAGAAATTGGCTACGATA	1647
CYP52D4A	1346	GATGTGGCGCACGGGGTTTTTGTGTTGGCGAGTCTGTGGGTCGTTTGAAGACGAAGATCGGAGG-----	1408
		** ** * * * * * ** * * * * *	
CYP52A1A	1838	CTCCAAACGAAA-----TCCACGGAAGAGAAACTTTGGCGCTGCTTTCAACGTTTCCCAACACTACTTTGGC	1904
CYP52A2A	1857	TCAATGCGCTTGACTTTTGACGGCAAGGCTGGCTTTGCTGATGCTTTTAACTATTTCGAGAAATTATTGGC	1926
CYP52A2B	1730	TCAATGCACCTTGACTTTGACGGCAAGGCTGGCTTTGCTGATGCTTTTAACTATTTCGAGAACTATTGGC	1799
CYP52A3A	1938	CAACACCACGAATTTTCGATGTCGACGAGAGATTTTCGTCGACGCTTTCAACTATTTCGAGACTTACCGGC	1907
CYP52A3B	1625	CAACACCACGAATTTTCGATGTCGACGAGAGATTTTCGTCGACGCTTTCAACTATTTCGAGACTTACCGGC	1694
CYP52A5A	1746	AAGACGATATAGATTTTCTGCTGAGAAAGGACTTTTCTGAGTCGTTCAACAAAGCCACGGAATTAATTGGC	1315
CYP52A5B	1785	AAGACGATATAGATTTTCTGCTGAGAAAGGACTTTTCTGAGTCGTTCAACAAAGCCACGGAATTAATTGGC	1854
CYP52A8A	1095	CGAAAGACATGT---CTGAAGAAAGACGCGAATTTGCCGACGCGTTCAACAAAGCCACGGAATTAATTGGC	1161
CYP52A8B	1648	CGAAGGACATGG---CTGAAGAAAGACGCGAATTTGCCGACGCGTTCAACAAAGCCACGGAATTAATTGGC	1714
CYP52D4A	1409	-----TTCCTGGAGACATTCAATGATGTCGACAGAGTATTTTGGC	1445
		** * * * * * * * * * *	

FIG. 15F-2

CYP52A1A	1905	CACCAGAGTTACTCCGAGCTTTTACTTTTGTGACCAACCCTAAGAAATTCAGAGACTGTAAACGCCAAG	1974
CYP52A2A	1927	TTTCGAGAGCGGTTATGCAACAATTTGACTGGGTGTGAACGGGAAAAAGTTTAAAGGAGTGCACCGCTAAA	1996
CYP52A2B	1800	TTTCGAGAGCGGTTATGCAACAATTTGACTGGGTGTGAACGGGAAAAAGTTTAAAGGAGTGCACCGCTAAA	1869
CYP52A3A	1908	CTACAGATTTTTTGTGCAACAAATGTACTGGATTTGAAATGGCTCGGAATTCAGAAAAGTCGATTGCTGTC	1977
CYP52A3B	1695	CTACAGATTTTTTGTGCAACAAATGTACTGGATTTGAAATGGCTCGGAATTCAGAAAAGTCGATTGCTGTC	1964
CYP52A5A	1816	TATTAGAACCCTTGGTGCAGACGTTCTACTGGTTGGTCAACAACAAGGAGTTTAGAGACTGTACCAAGCTG	1885
CYP52A5B	1855	TATTAGAATTTGGTGCAGACCTTCTACTGGTTGGTCAACAACAAGGAGTTTAGAGACTGTACCAAGCTG	1924
CYP52A8A	1162	CACCAGAGTTGCTTTTACAGAACTTGTACTGGTTGGTCAACAACAAGGAGTTCAAGGAGTGCATGCACATT	1231
CYP52A8B	1715	CACCAGAGTTGCTTTTACAGAACTTGTACTGGTTGGTCAACAACAAGGAGTTCAAGGAGTGCATGCACATT	1784
CYP52D4A	1447	AAC TAGGGCAACGTTGCAGAGTTGTACTTTCTTTCTGTGACGGGTTTAGGTTTCGCCAGTCAACAAGGTT	1516

FIG. 15F-3

FIG. 5G-1

CYP52A1A	2115	ATTGTTGAACATTATGTTGTCGCGAAGAGACACCACTGCCGGTGTGTTGCTCTTTCGTTTGTGTAATTG	2181
CYP52A2A	2131	ATTGTTGAACATCATGTTGCTGTGTAGAGACACACCGCGGTTGTGCTGTGTTTCTTCTGTAATTG	2200
CYP52A2B	2014	GTGTTTGAACATCATGTTGCCGTGTAGAGACACACCGCGGTTGTGCTGTGTTTCTTCTGTAATTG	2073
CYP52A3A	2112	GTATTTGAACATTTTGTGTCGCGTGTAGAGACACACCGCGGTTGTGCTGATTTGTTCTTCTAGAGTTG	2181
CYP52A3B	1899	GTGTTTGAACATTTTGTGTTGCCGTGTAGAGACACGACCGCGGTTGTGCTGTTGCTGTCTTCTAGAGTTG	1968
CYP52A5A	2020	GTCTTTTGAACATCTTGTGTCGCGAAGAGACACCACTGTGCGGTTGTGTCGTTCTGTCTGTCTTGTAGTTG	2089
CYP52A6A	2059	GTCTTTTGAACATCTTGTGTCGCGAAGAGACACCACTGTGCGGTTGTGTCGTTCTGTCTGTCTTGTAGTTG	2128
CYP52A8A	1366	GTCTTTTGAACATCTTGTGTCGCGAAGAGACACCACTGTGCGGTTGTGTCGTTCTGTCTGTCTTGTAGTTG	1435
CYP52A8B	1919	GTCTTTTGAACATCTTGTGTTGGCTGGAAGGACACCACTGTGCGGTTGTGCTCTTCTGTCTGTCTTGTAGTTG	1998
CYP52D4A	1642	AGCGTTGAACGTCCTTGTCTGTGACGCGACACCAACCGCGTGTGTTATTTATCTGTTTGCACCACTTTTGAAGCTTA	1711

CYP52A1A	2185	GCTAGACACCCAGAGATGTTGTCCTCAAGTTGAGAGAGAAGAAATCGAAGTTAACTTTTGGTGTGTTGGAGACT	2254
CYP52A2A	2201	GCCGAAGAACCCAGAGATTGTACCAACAACTTGAGAGAGAAATTCAGACACAAGTTTGGACTCGGTGAGAATG	2270
CYP52A2B	2074	GCCGAAGAACCCAGAGATTGACCAACAACTTGAGAGAGAAATTCAGACACAAGTTTGGTGTGTTGGTGAATG	2143
CYP52A3A	2182	TCGAGAACCCCTGAGTGTGTTGTTAACTTTGAGAGAGAGGTGGAACACAGATTTGGAATCGCGTGAAGAAG	2251
CYP52A3B	1969	TCGAGAACCCCTGAAAGTTGTTGCCAAGTTGTAGAGAGAGGTGGAACACAGATTTGGAATCGCGTGAAGAAG	2038
CYP52A5A	2090	GCCGACACCCAGAGATCTGGGCGCAAGTTTGTAGAGAGAAATTCGAACAACAGTTTGGTCTTGTGGAAGACT	2159
CYP52A5B	2129	GCCGACACCCACACATCTGGGCGCAAGTTTGTAGAGAGAAATTCGAACAACAGTTTGGTCTTGTGGAAGACT	2198
CYP52A8A	1436	GCCGAGAACCCACATCTGGGCGCAAGTTTGTAGAGAGAAATTCGAACAACAGTTTGGTCTTGTGGAAGACT	1505
CYP52A8B	1989	GCCGAGAACCCACATCTGGGCGCAAGTTTGTAGAGAGAAATTCGAACAACAGTTTGGTCTTGTGGAAGACT	2058
CYP52D4A	1712	GCCCGGAATGACCACTGTGAGAGAGAGCTACGAGAGAGTT-----ATCCCTGA--CGATGGGACCG	1771

FIG. 15G-2

[illegible]

FIG. 15G-3

CYP52A1A	2325	CTTGCGTATGTA	CCCATCTGTTCTCTGTC	AACTTTAGAACCGCCAC	CAGAGACACCACTTTGCCAAGAGGT	2394
CYP52A2A	2341	CTTGAGATTGTA	CCCATCCGTGCCACAGAA	TTTCAGAGTTGCCACCA	AAACACTTACCCCTCCCAAGAGGT	2410
CYP52A2B	2214	TTTGAGATTGTA	CCCATCCGTGCCACAGA	ATTTACAGAGTTGCCAC	CAAAACACTTACCCCTCCCAAGAGGT	2283
CYP52A3A	2322	CTTGAGATTGTA	CCCATCCGTGCCACAGA	ATTTACAGAGTTGCCAC	CAAAACACTTACCCCTCCCAAGAGGT	2391
CYP52A3B	2109	CTTGAGATTGTA	CCCATCTGTTCCACACA	CACTTCAGAGTTGCCA	CAAGAAACACTTACCCCTCCCAAGAGGC	2178
CYP52A5A	2230	CTTGCGTATTTA	CCCAAGTGTCCCAAGAA	ACTTCAGAACTCGCC	CAACAGAACACGACATTCGCCAAGGGGC	2299
CYP52A5B	2269	CTTGCGTGTTTA	CCCAAGTGTCCCAAGAA	ACTTCAGAACTCGCC	CAACAGAACACGACATTCGCCAAGGGGT	2338
CYP52A8A	1576	TTTGAGATTACA	CCCAAGTGTCCCAAGAA	CCGCAAGATTTGCGAT	TAAAGACACGACTTTACCAAGAGGC	1645
CYP52A8B	2129	TTTGAGATTACA	CCCAAGTGTCCCAAGAA	CCGCAAGATTTGCGAT	TAAAGACACGACTTTACCAAGAGGC	2198
CYP52D4A	1840	TCCTCGACTATA	CCCAAGTGTGCTAGGAA	CGCGATTTGCTACGAG	GAATACGACGCTTCCTCGTGGC	1909
		* * *	*****	** **	***	***
CYP52A1A	2395	GGTGGTGCTAA	CGGTACCGACCCCAAT	CTACATTCCTAAAGGCT	CCACTGTTGCTTACGTTGCTTACAGAA	2464
CYP52A2A	2411	GGTGGTAAGGA	CGGGTTGTCTCCTG	TTTGGTGAGAAAGGGT	CAACCGGTTATTTACGGTGTCTACGAG	2480
CYP52A2B	2284	GGTGGTAAGGA	CGGGTTATCTCCTG	TTTGGTGAGAAAGGGT	CAACCGGTTATTTACGGTGTCTACGCTG	2353
CYP52A3A	2392	GGTGGTGAAGA	TGATGATCTCGCC	AATGTGCTCAAGAGGGT	CAAGTTGTCATGTACATCTGTTATTGCTA	2461
CYP52A3B	2179	GGTGGTGAAGA	CGGATGCTCGCCA	ATTGTTGTCAGAAAGGGT	CAAGTTGTCATGTACATCTGTTATTGCTA	2248
CYP52A5A	2300	GGTGGTTCAGA	CGGTACTTCGCCA	ATCTTGATCCAAAGGGAGAG	AGCTGTGCTGATGTGATCAACTCTA	2369
CYP52A5B	2339	GGTGGTTCAGA	CGGTACCCAGCC	AATCTTGATCCAAAGGGAGAG	AGCTGTGCTGATGTGATCAACTCTA	2408
CYP52A8A	1646	GGTGGCCCCAA	CGGCAAGGATCC	TATCTTGATCAGGAAGGAT	CGAGTGGTGCGTACTCCATCTCGGCAA	1715
CYP52A8B	2199	GGTGGCCCCAA	CGGCAAGGATCC	TATCTTGATCAGGAAGGAT	CGAGTGGTGCGTACTCCATCTCGGCAA	2268
CYP52D4A	1910	GGAGGTCGAGA	TGGATCGTTTCGGA	TTTGTAGAAAGGCGCAG	CGAGTGGGTATTTTCAATTTGTGCTA	1979
		** **	** *	*	**	**

FIG. 15H-I

FIG. 15H-2

CYP52A1A	2605	GCCTTGACTGAAGCTTCTTAATGTGATCACTAGATTGGCCCCAGATGTTGAAACTGTCATCTGATCCAG	2674
CYP52A2A	2621	GCCTTGACACAAAGCTTCGTAATGTCACCTGTCAGGTTGCTCCAGGAGTTTGACACACTTGCTATGGACCCAG	2690
CYP52A2B	2494	GCCTTGACACAAAGCTTCGTAATGTCACCTGTCAGATTGCTCCAGAGTTTGGACACTTGTCTATGGACCCCA	2563
CYP52A3A	2602	GCCTTGACCCGAAGCTTCATACGTCACTGTCAGATTGCTCCAGGAGTTTGACACTTGTCTATGGACCCCA	2671
CYP52A3B	2389	GCCTTGACTGAAGCTTCATACGTCACTGTCAGATTGCTCCAGAGTTTGGAACTTGTCCCTGGATCCAA	2458
CYP52A5A	2510	GCCTTGACCGAAAGCTGGCTAATGTTGGTTAGATTGGTGCAAGAGTTCTCCACATAGGCTGGACCCAG	2579
CYP52A5B	2549	GCCTTGACCGAAAGCTGGTTACGTTTGGTTAGACTTGGTTGCAAGAGTTCTCCACATAGGCTGGACCCAG	2618
CYP52A8A	1856	GCTTTGACCGAAAGCCGGTTACGTTTGGTTAGACTTGGTTGCAAGAAATCCCTAGCTTGTTCACAGACCCCG	1925
CYP52A8B	2409	GCTTTGACCGAAAGCCGGTTACGTTTGGTTAGACTTGGTTGCAAGAAATCCCTAGCTTGTTCACAGACCCCG	2478
CYP52D4A	2120	GCAATCCCTTGAAGCTTCGTAATGTTTGGCTCGATTACACAGATGCTACACGAGATACAGCTTAG--AA	2186

FIG. 15H-3

CYP52A1A	2675	GTCTCGAATACCCCTCACCAAGTGTATTCACTTGACCATGAGTCAACAGATGGTGTCTTTGTCAAGAT	2744
CYP52A2A	2691	ACACCGAATATCCACTAAGAAAATGTGCGCATTTGACCAATGTCGCTTTTCGACGGTGCCAAATTTGAGAT	2760
CYP52A2B	2564	ACACCGAATATCCACTAGGAAAATGTCGCAATTTGACCATGTCCTTTTCGACGGTGCCAAATTTGAGAT	2633
CYP52A3A	2672	ACACCGAATATCCACCAAAATTCAGAACACCTTGACCTTTGTGCTCTTTTGATGGTGTGATGTTAGAAT	2741
CYP52A3B	2459	ACGCTGAGTAGCCCAACCAAAATTCAGAACACCTTGACCTTTGTGCTCTTTTGATGGTGTGACGTTAGAAT	2528
CYP52A5B	2619	ATGAAGTGTATCCCAAGAGAGGTTTGACCAACTTTGACCATGTGTTTCGAGGATGGTCTATTGTCAAGTT	2649
CYP52A5A	2580	ACGAGGTGTACCCGCCAAGAGAGGTTTGACCAACTTTGACCATGTGTTTCGAGGATGGTCTATTGTCAAGTT	2688
CYP52A8A	1926	AAACCAAGTAGCCACCACTAGATTGGCACACTTGACGATGTGCTTTGTCAGGGTGACACGTCGAAGAT	1995
CYP52A8B	2479	AAACTGAGTAGCCACCACTAGATTGGCACACTTGACGATGTGCTTTGTCAGGGTGACACGTCGAAGAT	2548
CYP52D4A	2187	CTACCGAGTAGCCCAACCAAGAACTCGTTCACTCACGATGAGTCTTCTCTCAA CGGGGTGTACATCCGAC	2256
		*** ** *	
CYP52A1A	2745	GTAA-AGTAGTCGATGCTGGGTAATTCGATTACAATGT--GTATAGGAAGATTTTGGTTTTTTTATTCGTCTCT	2811
CYP52A2A	2761	GTATTAGAGGGTCATGTGTATTTT-GATTTGTTA-----GTTTGTAAATTACTGATTAGGTTAATTCATG	2824
CYP52A2B	2634	GTATTAGAGGATCATGTGTATTTTGAATTTGGTTTGTAGTCTGTTGTGATGATTTGATTTAGTTAAATTCACG	2703
CYP52A3A	2742	GTACTAAGTTGCTTTTCTCTGCTAAATTTCTCTGATAGTCTGTGTATTTAAATTTGAATCGGCAATG	2811
CYP52A3B	2529	GTTCTAAGGTTGCTTATCTCTGCTAGTGTATTT--TATAGTTTGTGTATTTAAATTTGAATCGGCAATG	2595
CYP52A5A	2650	TGACTAGCGGGCGTGGTAATCGTTTGATTTTGTGA--GTTTCTGTTTTCGAGTAATGAGATACTATTCA	2716
CYP52A5B	2689	TGACTAGTA-CGTA-TGAGTGGTTTGTATTTGTGA--GTTTCTGTTTTCGAGTAATGAGATACTATTCA	2753
CYP52A8A	1996	GTCAATAGGTTTJCCC---CATACAAGTAGTTCAGTA---AATATACACTGTTTTTACTTCTCTTCATACC	2059
CYP52A8B	2549	GCAATAGGTTT-----TGCTTTCAGCTTTGTTTCCATA--	2580
CYP52D4A	2257	TAGAACTTTGATTTATGTGTTTTATGTTTAATCGGGGCAAGCACTGCAAGTCATTGATGTTTGTGGAAGCCC	2326

FIG. 151-I

CYP52A1A	2812	TTTATTTAAATTTTGTATAAATTAG-TTTAGAGATTTCAATTAATACATAGATGGGTGCTATTTCCGAACCT	2880
CYP52A2A	2825	GATTTGTTATTTATGATAGGGTT-----TGCGCGTGTGCAATTCACCTCGGAGTCGTTCCAGGTG	2885
CYP52A2B	2704	ATTGTTATTTATGATAGGGGTGGGTGTGTGTGTGTGTGCTATTCACATCGGATGCTTCGAGTTG	2773
CYP52A3A	2812	ATTTTCTGATACCAATCAACGTA-----GTGCGATTTGACCAAAACCGTTCAAAAGTTTGTGTTCTC	2873
CYP52A3B	2596	ATTTTCTGGTACTATAACTGTA-----GTGGGTTTTGACCAAAACCGTTCAAAAGTTTGTGTTCTC	2657
CYP52A5A	2717	GATAAGCGAGTCGATGTACGTTT-TGTAAGAGTTT--CCT-TACAAACCTTGTTGGGG-TGTGTGAGGTT	2781
CYP52A5B	2754	GATAAGCGGGTGGATGTACGTTT-TGTAAGAGTTT--CCT-TACAAACCTTGTTGGG-TGTGTGAGGTT	2817
CYP52A8A	2060	AAATGACAAAGATTTTAAGCATG-CCTAACAGTGACCG-GACAAATGTGTGCGCATGTATGTATCAACA	2127
CYP52A8B	2581	-----TGCAAGT	2587
CYP52D4A	2327	AGCAATTTGGTTCGGGAGCATCAATTAACCAAATGCTCTTGAAGGGTTTGATTTCTTGACCTTCTCTCTCT	2396
CYP52A1A	2881	TTACTTCTATCC--CCTGTATCCCTTATTAATCCCTCTCAGTCACATGATTCGTGTAATTTGTCGTGACGA	2948
CYP52A2A	2886	ATGTTTCTTCCATCT--GTGAGGTCAAAGAGTTTGTGTTTGTAACTCCGGACGATGTTTTAAATAG	2953
CYP52A2B	2774	TGTGTTCTTCCATCCT--GTTCAGATCAAAGAGTTTGTGTTTGTAACTCCGGACGATGCTTAGATAG	2841
CYP52A3B	2658	TGCTCGCTCATCAGCAGCTGTTTGTGAAGACGAAAGA-GAAAAATTTTGTGTA	2930
CYP52A5A	2782	TATTTTCCCTCCATCTTCGTGCTCGCTCATCAGCAGCTGTTTGAAGACGAAAGAAATTTTGTGTA	2727
CYP52A5B	2818	G----CATCTTAG-GAGAGATATGACACTTTTG-CAGCTCTCGGTATACAGTTTCTTTGTAACCTC	2849
CYP52A8A	2128	ATTGTAAAAATAG-TGTACACTAAATTTGTGTCGCGCGGATAAATACAGTTTGGTTTGTGTAAACCTC	2881
CYP52A8B	2588	AGTTCAGTAAT--TACACACTAAATTTGTGTCGCGCGGATAAATACAGTTTGGTTTGTGTAAACCTC	2654
CYP52D4A	2397	-----TGCAAGT	2463

FIG. 15I-2

CYP52A1A	2949	CACAACTCCCTAACGGACTTAAACCATAAACAGCTCAGAACCATAGCCGACATCACTCCTTCTCTC	3018
CYP52A2A	2954	AAGGTCGATCTCCATGTGATTGTTTGACTGTTACTGTGATTATGTAAATCTGCG-----GACGTTATA	3016
CYP52A2B	2842	AAGGTCGATCTCCATGTGATTGTTT-GACTGCTACTCTGATTATGTAAATCTGTAAAGCCTAGACGTATATG	2910
CYP52A3A	2931	AACAACACTGTCCAAATTTACCCAAACGTGAACCATTAAG--CAAAATGACGGGCC-----CTTTCAA	2989
CYP52A3B	2728	AACAACATGCCCAACTTACCCAAACGTGAACCATTAACCAAAATGACGGCG-----CTTTCAA	2788
CYP52A5A	2850	TATCAATCATGTGGGGGGGGTTCAFTGTTGGC-CATGGTGGTGCAATGTTAAATCCGCC-AACTACC	2917
CYP52A5B	2882	TGCCAATCATGTGG-----GGATTCAATGTTTGCC-CATGGTGGTGCAATGTTAAATCCGCC-AACTACC	2944
CYP52A8A	2197	GCGGATATCTCTGGC-----AGTTTCTCTCTCCGC-AGCAGCTTTGCCACGGGTTTGCTCTGGGGCCAA	2260
CYP52A8B	2655	TCGGACATCTCTGGT-----GGTTTCCCTTCTCCGC-AGCAGCTTTGCCACGGGTTTGCTCTGGGGCCAA	2718
CYP52D4A	2464	TAACCGCATCTGGAGTA---TCTCGCCGTCGTTCAAGTAG--CACGAAACACGACGCTCACCATCTG	2528

FIG. 15I-3

CYP52A1A	3019	TCCTTCTCCAAACCAATGACATGGACAGACCCACCCCTCCTATCCGAATCGAAGACCCCTTATTGACTCCATAC	3088
-CYP52A2A	3017	CAAGCATGTGATTGTGGTTTT-----GCAAGCT-TTTCGACGACAAATGATGTCGACGATTACGTAA	3079
CYP52A2B	2911	CAAGCATGTGATTGTGGTTTT-----GCAAGCTGTTTTCGACGACAAATGATGTCGACGATTACGTAA	2975
CYP52A3A	2990	CTGGTCTGCTGGAAGCATTCGGG-----GATATCTCAACGCCCTTAAGTTTGAACAGACATTTGATTAG	3054
CYP52A3B	2789	CTGGTCTGCTGAGGCATTCGGG-----GATATCTCAACACCCCTTAAGTTTGAAGGAAGACATTTGATTAG	2853
CYP52A5A	2918	CAATCTCACATGAAGCACTAAGCACAATAAAAAAAGATGTTGGGGGAAACCTT-TGGTTTCCCTTC	2986
CYP52A5B	2945	CAATCTCACATGAAGCACTAAGCACAATAAAAAAAGATGTTGGGGGTTCTT-TTGATG-----	3005
CYP52A8A	2261	CAAAATCCAAAGGGGG-----AGAACTTAAACACCCCTTATCTCCACCTC-TAGGTTGTAGCT	2318
CYP52A8B	2719	CAAAATTCGAAAGGGGGGGGGGGGAGAAAGTTAACACCCCTGTTC--CACCG-TAGGCTGTAGCT	2785
CYP52D4A	2529	CTTCCCAATCTTGACACCC-----ACAGATACCCCTCGGGCTTCAATGGATCAAAAAAGTCGGCAACC	2590
CYP52A1A	3089	CCACTGGAGGCCCTCAAGCCACACACGTCATCCAGCCACCCATCAACACATCCCTCTACTCGACAAC	3158
CYP52A2A	3080	TCCTTTGTTA-----GAGGGGTAAAAAATAAAATGAGCCAGCAGAAATTTCAAACAATTCGCAAAACAATG	3144
CYP52A2B	2976	TCCATATTAT-TTAGAGGGGTAAATAAAATAAA-TGGCAGCCAGAAATTTCAAACAATTTGCAAAACAATG	3043
CYP52A3A	3055	ACACCATAGA-TTTCAGCGGCATCAAGATGACC-----TTGCCCCACATTTTGACGACCCCAACACCATG	3119
CYP52A3B	2854	ACACCATAGA-TTTCAGCGGCATCAAGATGACC-----TTGCCCCACATTTTGACGACCCCAACACCATG	2918
CYP52A5A	2987	TTAGTAAT--AAACACTCTCACTCTCACTCTCACTCTCACTCTCACTCTCACTCTCACTCTCACTCTCACTCT	3054
CYP52A5B	3006	TTGGGGAAA--ACTTTCGTTTCTTCTCACTCTCACTCTCACTCTCACTCTCACTCTCACTCTCACTCTCACTCT	3073
CYP52A8A	2319	CTTGTGGGG--ATGCAATTTGTCGACGTTTTTTATGTTTTGTCTAGATTTTGTAGATTTGATGATTGATTTTC	2386
CYP52A8B	2786	CTTGTGGGGGATGTAATTTGTACGTTTTTC-ATGTTTGGCCAGACTTTGATGGATGATGATGATGATGATGATG	2854
CYP52D4A	2591	CCGCGTATATGTTCATGTAAATCTCCATGGCCACT--CCATCAACACACACTGTATGGAGCGACTGACGGTG	2658

FIG. 15J-I

CYP52A1a	3159	GTCCAAAGACGCGGAGTTCTTGTTGTCCCGGAAATCAGCATCCCGGCCACATACAGCAGCGCTTGATT	3222
CYP52A2a	3145	CAAAAAATGGAAACTC---CAACAGAAAAA-AAAAAAATCCGACAGCTCCGAGACCCACAGAAACTG	3211
CYP52A2b	3044	AAAAAGATGAGCACTC---CAACAGAAAAA-AAAAAAATCCGACAGCTCCGACACCAACAAACAATG	3111
CYP52A3a	3120	GAAAGATCAGCCACA---AACTAGCGCATGATCAAGCGCTGTGACCTTTGCCCAATGGAGAGCAAGTG	3185
CYP52A3b	2919	GAAGAAATCGGCCAGA---AACTAGCGCATGATCAAGCGCTGTGCGCTTTGCCCAATGGAGAGCAAGTG	2984
CYP52A5a	3055	AGACACCCAGAAAAAAGAAACAAATCCAGATAGAAAAAACAAGGCT--GGACACCATATAAT--AAAC	3122
CYP52A5b	3074	AGACAAACAGAAAAA---CAAATCCAGATAGAAAAAACAAGGCT--GGACACCATATAAT--AAAC	3135
CYP52A8a	2387	TTATGTCGTAGGCGGTG---CTTGAAGAAGTGTCAAATGTGACAGCGC--ACGCTATTTCGACAT--GAAC	2450
CYP52A8b	2855	TTATGTCGTAGGCGGTG---CTTGAACAAGTGTCAAAGGTGACAGCGC--ACGTTATTTCGACAT--GAAC	2918
CYP52D4a	2659	CCACCACCTGCCCTCG-----TTGAGTCAAGCGCATGATGCCGGGATCCAGTACTCTCAATGGGAACC	2722
CYP52A1a	3229	CGCTGCATATCTCGCGCAGCCCAACAATGGGAGCATATGTGACCTTTTGA---CGACTAAACGCTATTCACGAG	3298
CYP52A2a	3212	GGG---CGCGCAGAAATATTGACATATTGTGACCTTTTGA---CGACTAAACGCTATTCACGAGT	3266
CYP52A2b	3112	GGGG--CGCGCAGAAATATTGACATATTGTGACCTTTTFTT---ATTTTTCGGTTAACTTTCANTGCACTG	3177
CYP52A3a	3186	GAGTTGAACCAAGGCTCTTAGAAGTTACCAATATTGTGCAATGAGTTTGTGACCTTGACCAATATTGAACG	3255
CYP52A3b	2985	GAGTTGAACCAAGGCTCTTAGAAGTTACCAATATTGTGCAATGAGTTTGTGACCTTGACCAATATTGAACG	3054
CYP52A5a	3123	AACATAGGCTACATCGATCTCCACGTTTCTCTCTGACAGCTTAGCT--AACAAACAACACTCACTTCA	3191
CYP52A5b	3136	AACATAGGCTACATCGATCTCCACCTTTTCACT---TCTTCTCTTCAGACTTATCT--AACAAACAGCTCACTTCA	3201
CYP52A8a	2451	CGCAAAAGGTTAATTGCAATCAATACAG--GGGTGCTCTGTGCTTAG---ATTGGCAGCTCTGAGTTGCT	2515
CYP52A8b	2919	GCAAAAGGTTAATTGCAATCAATACAG--GGGTGCTCTGTGCTTAG---ATTGGCAGCTCTGAGTTGCT	2983
CYP52D4a	2723	TCT-----GACCGGTGTGCTGCAGTTTTCGAGGGGCGGATTTTCGA-----TCCATGATGTTCTTTGG	2779

FIG. 15J-2

CYP52A1A	3368	ACGACTTCGGTGGGTGTTATCTAAACGAAGATTCTATGAGACGACGATGTGTTTCGGTTTCGAGGATTG	3437
CYP52A2A	3329	TAACGTTCGCCCGGTCAACTCAATTTGAC-----G--AGTAACTTCCTTAAGCTCGAATTATGC	3385
CYP52A2B	3247	TAACGTTCGCCCATATCAACTCAATTTATC-----CTCATTCATGTGATAAAGAGAGGCCAAA	3305
CYP52A3A	3325	GATTTCCTTATTATTGAGAGCAAACTAC-----ATCTTGAACATACTTGGGTATTGTAT	3379
CYP52A3B	3124	GATTTCCTTACTATTGAGAGCAAACTAC-----ATCTTGAACATACTTGGGTATTGTAT	3178
CYP52A3A	3259	G-ACATCCGAACACGACCTCCAGCT-----TGAAAGAAATCAACACCGGCATCCAGAGGACGACTT	3321
CYP52A5B	3269	G-ACCATCCAGAACCGACCTCCAGCT-----TGAAAGAAATCAACACCGGCATCCAGAGGACGACTT	3331
CYP52A8A	2580	GCACATTCCGTTGTTCAATATTTCTC-----CTTCCCATGTTCCAGGGTTA--TC	2629
CYP52A8B	3049	GCACATTCCGTTGTTCAATATTTCTC-----CCCCCTGCTTCCCCCATTTGTTCCAGGGATTA--TC	3110
CYP52D4A	2848	GGGTGCTTGGTTTGCAAGCTCTTCGATCG-----AGCGTAGTGAGTAGACAGTTGGCGGG	2901
CYP52A1A	3438	TGCGTACGTGATGTGTCCTTTTGTGATGACCCAGAGGAAGTTACGTGTTGGGACGTACAGATCC	3507
CYP52A2A	3386	AGCT--CGTGCCTCAACCTATGTGCAGGAAAGAAATTCAAAA--AATCGAAA--ATGCGACTTTCGAT	3451
CYP52A2B	3306	AGCT--AAT--TGGCAGACCCCAAGGGGAAACAGGAGTAGAAGC--AATGGAAACACGCCCATGACAGT	3371
CYP52A3A	3380	TTCCG--AAGCAGGATGTTGATTGTAGTACCGGACACACGCGCT--TGTTGATAGTATTTTGAAGAAGT	3446
CYP52A3B	3179	TTCCG--AAGCAGGATGTTGATGTAGTACCGGACACACGCGCT--TGTTGATAGTATTTTGAAGAAGT	3245
CYP52A5A	3322	TGCC--AAGTTGTTGTCTGCCACCCCGAAAATCCCAACCAAGCA--AGTTGAACGGCACCCAGCAATT--	3387
CYP52A5B	3332	TGCC--AAGTTGTTGTCTGCCACCCCGAAAATCCCAACCAAGCA--AGTTGAATGCCAACCCAGCAATT--	3397
CYP52A8A	2630	AACA--ACGTTGCGGCTCTCTCTCCCGCCCTCCCGCCAGTTAT-----GTACAAAGAAATTAATTT--	2674
CYP52A8B	3111	GGTGTGCTCGGCTTTATTTCTGTGTTGTGTTTCTCTTAGT--CTTGGAAATGACGCTGTTATCGAC	3171
CYP52D4A	2902		2969

FIG. 15K-1

CYP52A1A 3508	ATTGAAAGTTGAGCTGGGTAAAGACGGGACGTGGA-GTGGACCATGG---CGACGAGCTCGGATCCT	3573
CYP52A2A 3452	TTTGAATAAACCAAAAGAAATGTCGATCTTTTTC-----TGGCTCTCGCTCTCTCGACCCAAATCA	3516
CYP52A2B 3372	GCATTTAGCCACACA---ACACATCTAGTATTCTTTT-----TTTTTTTGTGGCAGGTGCACACCTGG	3433
CYP52A3A 3447	TTTGAAGAATCTAC-----AAGTTGATAAGCGTGTGA-----ACGATATGATTGACAAGCAAAAGGTGA	3507
CYP52A3B 3246	TTTGAAGAAGATCTAC-----AAGTTGATAAGCGTGTGA-----ACGATATGATTGACAAGCAAAAGGTGA	3306
CYP52A5A 3388	GTCTGAGGTGCGCCATTGCCAAAAGGAGTACGAGTGTGATTTGCTTGACGACGCCACAAAAGACCCA	3457
CYP52A5B 3398	GTCCGAAGTCGCCATTGCCAAAAGGAGTACGAGTGTGATTTGCTTGACGACGCCACAAAAGACCCA	3467
CYP52A8A 2675	GTCCGACGGCACCGATCTCTCAAGATACAGATAA-----ACCTTAAATCTGCAAAAACAAGACCCC	2736
CYP52A8B 3172	GTCCGACGGCACCGATCTCTCAAGATACAGATAA-----ACCTTAA-----TCC	3216
CYP52D4A 2970	GGTTCTGTAGTATAAGTAGCGCCATATGAGAAATGTATA-----TCCGCATCACCCAGACTCTTCAGCCT	3034
CYP52A1A 3574	GGTGGGTTTATCCCGCA-ATGATTAACCTGATTTGAGCA-TCCCTGGAGCAATCGCAAAAGATGTGCCTAG	3641
CYP52A2A 3517	CAACAAATCTCGCGCAGTATTTGAGCAAAAC--CACAAACAATAAAAAAACAATTTCTACACACT	3584
CYP52A2B 3434	ACTTTAGTTATTGCC-CAATAAGTTAACATCT--CACCTTTGGCTCTCCAGTGTCTCGCTCCAGA	3500
CYP52A3A 3508	CAAGCAGCATCAACAGTCTAGCATTCATCAATTG--CATCAACTCTCGAGAGGTCAACTATTCTCGCA	3575
CYP52A3B 3307	CAAGCAGCATCAACAGTCTAGCATTCATCAATTG--CATCAACTCTCGAGAGGTCAACTATTCTCGCA	3374
CYP52A5A 3458	ATCAAGTCACTCCAGATCAAGATCTTGTATTTGATTTGACAAGTTCAAGGTGACTTGT---TTGAGTTGCCG	3524
CYP52A5B 3468	ATCAAGTCACTCCAGATCAAGATCTTGTATTTGATTTGACAAGTTCAAGGTGACTTGT---TTGAGTTGCCG	3534
CYP52A8A 2737	TCCCCATAGCCTAGAGACACAGAGATGATGGAGCACTCTCCAGTACTGGTACATCGCACTCTCTG	2806
CYP52A8B 3217	TCCCCATAGCCTAGAGACACAGAGATGATGGAGCACTCTCCAGTACTGGTACATCGCACTCTCTG	3286
CYP52D4A 3035	GTTCACACGACTGAGGCTGTGTGGCCGTGTGACCAATTGGTTTCTTTTGGTGACCTAGATTGGTCCCGCAGG	3104

FIG. 15K-2

CYP52A1A	3642	TG---TATTAAC	TACATACAGAAATAAAACGTCTCTTGATTCATTGGTTT---GGTCTCTTGTGGGT	3705
CYP52A2A	3585	T---CTTTTCT	TACCAAGTCAACAAAAACAACAAATATACACCATTTCAACGATTTTGCTCTTAT	3650
CYP52A2B	3501	TG---CTCGTTT	TACCCCTCGAGCTAACGACACACACACACCCCATGAGGGGAATGGCAAGTT-----	3562
CYP52A3A	3576	CA---CGAAC	CTTTTGGG-ACCTGGTTTGTGTGGATTGGTTGGTTGACAACTATTTCAACACAGTTTGGCATTTA	3641
CYP52A3B	3375	CA---CGAAC	CTTTTGGG-ACCTGGTTTGTGTGGATTGGTTGGTTGACAACTATTTCAACACAGTTTGGCATTTA	3440
CYP52A5A	3525	AC---CAGAA	GTTCCTCTACTCCATCGTGTCCAACTCCGTCAACATCGCCCC-TGGACCTTGTCTCGGG	3590
CYP52A5B	3535	AC---CAGAA	GTTCCTCTACTCCATCGTGTCCAACTCCGTCAACATCGCCCC-TGGACCTTGTCTCGGG	3600
CYP52A8A	2807	TA---TG	GTTCATCTTGGCTTCCACGACGACGACGACCACTTACTTTG-CGCCACAAGCTCGGG	2872
CYP52A8B	3287	TA---TG	GTTCATCTTGGCTTCCACGACGACGACGACCACTTACTTTG-CGCCACAAGCTCGGG	3352
CYP52D4A	3105	GAAAGCA	AGGGCTGTAGGGGGCATACCAAAAGGTCGTGTATCATGTGCTTACCATGTG	3174

FIG. 15K-3

CYP52A1A	3706	CCGAGCCAAATATTTCACATCATCTCCTAAATCTCCAAGAAUCCAAAGTAGCGTAGTCCAGCAGCCCT	3775
CYP52A2A	3651	AAATGCTATATAATGGTTTAATTCAACTCAGGTATGTTAT-TTAACTGTTTTCAGCTCAAGTATGT--T	3717
CYP52A2B	3563	AAACACTTTTGGTTTCAATGATTCCTATTGCTACTCTCTGTTTGTGTTTGTGATTTGACCAATGT--G	3630
CYP52A3A	3642	GACAACTTACAAAGAGTATTGGCATTGATCTGAAGAACATCAGCATGAAGACATCTTGATCATAC--A	3709
CYP52A3B	3441	GACAACCTACAAAGAAATATTGGCAATTGATCTGAAGAACATCAGTATCAAGATATCTTGATCGTAC--G	3508
CYP52A5A	3591	AGAAGTTGACACCGGCTTGATCAACTTGGCCTTCCAGAACACAAAGACAGCACTTGGACGAGGTCAIT--G	3559
CYP52A5B	3601	AGAAGTTGACACCGGCTTGATCAACTTGGCGTTCAGAACACAAAGACAGCACTTGGACGAGGTCAIT--G	3569
CYP52A8A	2873	CGCGGTCATTCACGACACCCAGTACGACGGTGGTATGGGTTCAAGTTTGGCGGGAGTTTCTCAA--G	2940
CYP52A8B	3353	CGCGGCGGTTTCACGACACCCAGTACGACGGTGGTATGGGTTCAAGTTTGGCGGGAGTTTCTCAA--G	3420
CYP52D4A	3175	TGTGGTTGGGGGAAATTCGCCCATTTTGTGTAAAGAAAGTTCGTGGGTTCGTGAG-A	3243
CYP52A1A	3776	CTGAGATCTTATTTAATATCGACTTCTCAACACCGGTGGAATC--CCGTTCCAGACCAATGTTTACCTGTA	3843
CYP52A2A	3718	CAAAATCACTACTATTTTGATGTTTGTGCTTTTCTAGAAATCAAAACAGCCCAACAACGCCGAGCTT	3787
CYP52A2B	3631	AAATAACGACAATTATATACGTTT---TCGTCTGTCCTC---CAATGTCT-CTTTTGTGCCAAT	3692
CYP52A3A	3710	CTTCTCCCAATCGACACTACAAATGTTTAAAGCTGGTGGTTGGACAA-GAAAGACGAGCGCTGCAGTTGAACA	3778
CYP52A3B	3509	CTTCTCCCAATCGACACTACAAATGTTTAAAGCTGGTGGTTGGATAA-GAAAGACGAGCGCACTGTTGACCA	3557
CYP52A5A	3660	ACATCTTCAACGAGTTTATCGACAAAGTTCTTTGGCAACACGGAG--CCGCAATTGAC-----CAACTTCT	3722
CYP52A5B	3670	ACATCTTCAACGAGTTTATCGACAAAGTTCTTTGGCAACACGGAG--CCGCAATTGAC-----CAACTTCT	3732
CYP52A8A	2941	GCGAAGAAATTCGGGCGGACAGCGACTTGGTGCATGCGCGGTT--CCGTGGCGG-----CATGGACA	3001
CYP52A8B	3421	GCGAAGAAATTCGGGCGGACAGCGACTTGGTGCATGCGCGGTT--CCGTGGAGGGG-----CATGGACA	3484
CYP52D4A	3244	ATCTGTGTGAACCAATCCACCCGCAATTTCCGTTTGCCAAAGTGGAA-GAGCAATCAACCAACCTGCTTGTG	3312

FIG. 15L-1

CYP52A1A	3844	GTGTGTTTGCTTTGTTCTTGATGACAAATGATGATTAATTGTACAGATACCTGAAATAATAAACAATCCAGT	3913
CYP52A2A	3788	GTGCAATAGACGGTTTGTTTACTCATTAGATGGTCCAGAGTTACTTTTCAAGCCAAAGTCTCT- CGAGTT	3856
CYP52A2B	3693	TTGCTTTTGTCTTTTGTCTTTTGCACT- --CTCTCCCACTCCCACAATCAGTCAGCCACACACA- CAA	3755
CYP52A3A	3779	GTCTTCAAGTACATCATCTTCAACAGT- -GTCAAGAGACTACAACTCCAACATCGGCTCCACAGCCAAAG	3846
CYP52A3B	3578	GTTCTCAAGTACATCACTCAACAGT- -GTGCGAAGACTACAACTCCAACATCGGAGCCACAGCCAAAG	3645
CYP52A5A	3723	TGACCTTGTGCGGTGTGTGGACGGGTGTGATTGACCATGCC- AACTTCTTTGAGCGTGTCTCTCGGACCT	3791
CYP52A5B	3733	TGACCTTGTGCGGTGTGTGGACGGGTGTGATTGACCATGCC- AACTTCTTTGAGCGTGTCTCTCGGACCT	3801
CYP52A8A	3002	CCTTCTCGAGCTACATTTGCGGATCCATATCATCTTACC- CGGGACCCGAGAACATCAAGCCGGTCT	3070
CYP52A8B	3485	CTTTCTCGAGCTATACTTTGCGCATCCATATCATCTTACT- CGGGACCCGAGAACATCAAGCCGGTCT	3553
CYP52D4A	3313	CCCAATCAGCCATTCCCTCGGGAATATAAAATCAAC	3348
CYP52A1A	3914	CATTGAGCTTATTACTCGTGAACCTTAGAAAGAACTCATTCACCGGTTCCCAAAAACCCAGAAATTGAA	3983
CYP52A2A	3857	TTGTTTGTGCTGTTTCCCNATTCCTAACTATGAGGGTTTTTATAAGGTTCCAAAGACCCCAAGGCATAGTT	3926
CYP52A2B	3756	ATGATATCGATTGTGCCAAAACCAAACTCAGTGGCTTTGAGGTGTGTGACGAGTT	3755
CYP52A3A	3847	ATGATATCGATTGTGCCAAGCC	3900
CYP52A3B	3646	TCAAGATCTTCTTGAACCTTGGACTCGTATGTGGAC	3663
CYP52A5A	3792	TCAAGATCTTCTTGAACCTTGGACTCGTGTGTGGACAACTCGGACTTCTTGAAACGACGTGGAGAACTACTC	3826
CYP52A5B	3802	TGGCGACGACGTTTCGATGACTTCTCGCTCGGTGGGAGGATCAGGTTCTTGAGCCGTTGTGGGGTATGG	3871
CYP52A8A	3071	TGGCGACGACGTTTCGATGACTTCTCGCTCGGTGGGAGGATCAGGTTCTTGAGCCGTTGTGGGGTATGG	3140
DYP52A8B	3554	TGGCGACGACGTTTCGATGACTTTTCG	3579
CYP52D4A	3349		3348

FIG. 15L-2

CYP52A1A 3984	GATCTTGTCTCAACTGGTCATGCAAGTAGTAGATCGCCATGATCTGTGATACCTTTACCAAGCTATCCTCTCCA	4053
CYP52A2A 3927	TTTTTGGTTCCTTCTTGTTCGTG	3948
CYP52A2B 3756		3755
CYP52A3A 3901		3900
CYP52A3B 3669		3668
CYP52A5A 3827		3826
CYP52A5B 3872	CGACTTTTTGTACGACGAGCCGACGAGTACCAAGAACTT	3910
CYP52A8A 3141	GATATTACGTT	3152
CYP52A8B 3580		3579
CYP52D4A 3349		3348

FIG. 15L-3

CYP52A1A 4054	AGTTCTCCACGTACGGCAGTAGCGCAACGAGCTCTGGAAGCTTTGTTTGGGTCATA	4115
CYP52A2A 3949		3948
CYP52A2B 3756		3755
CYP52A3A 3901		3900
CYP52A3B 3669		3668
CYP52A5A 3827		3826
CYP52A5B 3911		3910
CYP52A8A 3153		3152
CYP52A8B 3580		3579
CYP52D4A 3349		3348

FIG. 15M

CYP52A1A	1	MATQEI	IDS	VL	PYL	-----	TKWY	VT	IT	AA	LV	FL	IS	TI	KN	YV	38
CYP52A2A	1	MTVH	DI	IAT	Y	-----	FTK	WV	IV	PL	AL	TA	YR	VL	DY	FG	35
CYP52A2B	1	MTAQ	DI	IAT	Y	-----	ITK	WV	IV	PL	AL	TA	YR	VL	DY	FG	35
CYP52A3A	1	MSSSP	SFA	QEV	LAT	TS	PI	EY	FL	DN	YR	WY	FI	PL	VL	SL	50
CYP52A3B	1	MSSSP	SFA	QEV	LAT	TS	PI	EY	FL	DN	YR	WY	FI	PL	VL	SL	50
CYP52A5A	1						MTB	Q	L	L	E	Y	-----	WY	VP	VL	30
CYP52A5B	1						MTB	Q	L	L	E	Y	-----	WY	VP	VL	30
CYP52A8A	1						MLD	Q	I	L	H	Y	-----	WY	IV	PL	30
CYP52A8B	1						MLD	Q	I	F	H	Y	-----	WY	IV	PL	30
CYP52D4A	1						MA	I	S	S	L	S	W	D	-----	V	32
CYP52A1A	39	KAKK	LC	VP	PP	YL	KD	AG	LT	GI	LS	IA	AI	KAK	ND	GR	85
CYP52A2A	36	LMYK	L	GAK	PP	FQ	K	T	D	C	F	G	KAP	LE	LL	K	82
CYP52A2B	36	LMYK	L	GAK	PP	FQ	K	T	D	C	F	G	KAP	LE	LL	K	82
CYP52A3A	51	LERR	F	HAK	PL	GN	VR	DP	T	F	GI	AT	PL	LI	YL	K	100
CYP52A3B	51	LERR	F	HAK	PL	GN	VR	DP	T	F	GI	AT	PL	LI	YL	K	100
CYP52A5A	31	LMK	L	GAA	P	T	N	KL	Y	DN	AF	GI	V	NG	WK	AL	77
CYP52A5B	31	LMK	L	GAA	P	T	N	KL	Y	DN	AF	GI	V	NG	WK	AL	77
CYP52A8A	31	LMK	L	GAK	PP	TH	V	Q	R	D	G	WL	G	F	G	R	77
CYP52A8B	31	LMK	L	GAK	PP	TH	V	Q	R	D	G	WL	G	F	G	R	77
CYP52D4A	33	LMH	K	G	A	R	E	I	EN	V	IND	OG	F	G	R	PL	79

FIG. 16A-I

CYP52A1A	86	PN--HTFYLSVAGALKIVMTVPDENIKAVLATQFTDPSLGTRSHAFAPLL	133
CYP52A2A	83	DRPDIPTFTFVFSINLVNTLEPENIKAILATQFNDFSLGTRHSHFAPLL	132
CYP52A2B	83	NRPDIPTFTFIPSINLISLEPENIKAILATQFNDFSLGTRHSHFAPLL	132
CYP52A3A	101	RDPKYKTIGLRIVGLPLIETMDPENIKAVLATQFNDFSLGTRHDFLYSLL	150
CYP52A3B	101	KDPKYKTIGLRIVGLPLIETIDPENIKAVLATQFNDFSLGTRHDFLYSLL	150
CYP52A5A	78	KNPSVGTVVSIILFCTRIVVTKDPENIKAILATQGFDSLGKRHTLFKPLL	127
CYP52A5B	78	KNPSVGTVVSIILFCTKIIVTKDPENIKAILATQGFDSLGKRHALFKPLL	127
CYP52A8A	78	ED----TFSSYAFGNHVVTRDPENIKAILATQGFDSLGSRVKFFKPLL	123
CYP52A8B	78	ED----TFSSYAFGNHVVTRDPENIKAILATQGFDSLGSRVKFFKPLL	123
CYP52D4A	80	PHPQNTLVNRLSVPVILT KDFVNI KAMLS TQFDDFSLGRLHQFAPLL	129
		.. * * ***** * * * * * * * *	
CYP52A1A	134	GDGIFTLLDGEGWKHSRAMLRPQFARDOI GHVKALEPHIQIMAKQIKLANQG	183
CYP52A2A	133	GDGIFTLLDGAGWKHSRAMLRPQFAREQI SHVKLLEPHVQVFFKHVRKAQG	182
CYP52A2B	133	GDGIFTLLDGAGWKHSRAMLRPQFAREQI SHVKLLEPHMQVFFKHVRKAQG	182
CYP52A3A	151	GDGIFTLLDGAGWKHSRTWMLRPQFAREQVSHVKLLEPHVQVFFKHVRKHKG	200
CYP52A3B	151	GDGIFTLLDGAGWKHSRTWMLRPQFAREQVSHVKLLEPHVQVFFKHVRKHKG	177
CYP52A5A	128	GDGIFTLLDGEGWKHSRAMLRPQFAREQVAHVTSLEPHFOLLKKHILKHKG	177
CYP52A5B	128	GDGIFTLLDGEGWKHSRAMLRPQFAREQVAHVTSLEPHFOLLKKHILKHKG	173
CYP52A8A	124	GYGIFTLLDAGWKHSRAMLRPQFAREQVAHVTSLEPHFOLLKKHILKHKG	173
CYP52A8B	124	GYGIFTLLDAGWKHSRAMLRPQFAREQVAHVTSLEPHFOLLKKHILKHKG	173
CYP52D4A	130	KGIFTLLDGPEWKQSRSMLRPQFAKORVSHI LLEPHFVLLRXHIDGNG	179
		* ***** **..*****. * * * * * * *	

FIG. 16A-2

CYP52A1A	184	KTFDIQELFFRFTVDTSATEFLFGESVHSLYDEKLGITPT-NEIPGRENFA	232
CYP52A2A	183	KTFDIQELFFRLTVDTSATEFLFGESVSLRDESIGMSINALDFDGKAGFA	232
CYP52A2B	183	KTFDIQELFFRLTVDTSATEFLFGESVSLRDESIGMSINALDFDGKAGFA	232
CYP52A3A	201	QTFDIQELFFRLTVDTSATEFLFGESAESLRDESIGLPTTKDFGRRDFA	250
CYP52A3B	201	QTFDIQELFFRLTVDTSATEFLFGESAESLRDSDSVGLTPTTKDFEGRGDFA	250
CYP52A5A	178	EYFDIQELFFRFTVDTSATEFLFGESVHSLKDESIGINQDDIDFAGRKDFA	227
CYP52A5B	178	EYFDIQELFFRFTVDTSATEFLFGESVHSLKDEETIGINQDDIDFAGRKDFA	227
CYP52A8A	174	EYFDIQELFFRFTVDTSATEFLFGESVHSLKDEEIGYDTKDMSEERR-FA	222
CYP52A8B	174	EYFDIQELFFRFTVDTSATEFLFGESVHSLKDEEIGYDTKDMAERRK-FA	222
CYP52D4A	180	DYFDIQELFFRFSMDVATGFLFGESVGLKDE-----D-----ARFL	216
		***** ** * .. * .. * .. * .. * .. * .. *	
CYP52A1A	233	AAFNVSQHYLATRSYSQTFYFLTNPKPRDCNKAHVHILAKYFVNKALNFT	282
CYP52A2A	233	DAFNYSQNYLASRAVMQOLYWLNGKKFKECNAKVHKFADYYVNKALDLT	282
CYP52A2B	233	DAFNYSQNYLASRAVMQOLYWLNGKKFKECNAKVHKFADYYVSKALDLT	282
CYP52A3A	251	DAFNYSQTYQAYRFLLOQYWLINGSEPRKSIADVHKFADHYVQKALELT	300
CYP52A3B	251	DAFNYSQTYQAYRFLLOQYWLINGAEPRKSIADVHKFADHYVQKALELT	300
CYP52A5A	228	ESFNKAQBYLAIRTLVQTFYVLVNNKEPRDCTKLHVKFTNYYVQKALDAS	277
CYP52A5B	228	ESFNKAQBYLSIRILVQTFYWLINNKPRDCTKLHVKFTNYYVQKALDAT	277
CYP52A8A	223	DAFNKSQYVATRVVALQNLVYLVNNKEFCENDIVHKFTNYYVQKALDAT	272
CYP52A8B	223	DAFNKSQYVLSRVVALQTLVYLVNNKEFCENDIVHKFTNYYVQKALDAT	272
CYP52D4A	217	EAFNKSQYLATRATLHELFLCDGFRFRQYKVRKVRKFCSCVHKALDVA	266
		***** * .. * .. * .. * .. * .. * .. *	

FIG. 16B-I

CYP52A1A 283 PEELEKSGYVFLYELVKQTRDPKVLQDQLINIMVAGRDTTAGLLSFA 332
 CYP52A2A 283 PEQLE-K-QDGYVFLYELVKQTRDQVLRDQLINIMVAGRDTTAGLLSFA 330
 CYP52A2B 283 PEQLE-K-QDGYVFLYELVKQTRDQVLRDQLINIMVAGRDTTAGLLSFA 330
 CYP52A3A 301 DDDIQ-K-QDGYVFLYELAKQTRDPKVLQDQLINILVAGRDTTAGLLSFA 348
 CYP52A3B 301 DDDIQ-K-QDGYVFLYELAKQTRDPKVLQDQLINILVAGRDTTAGLLSFA 348
 CYP52A5A 278 PEELE-K-QSGYVFLYELVKQTRDPNVLRDQSLINILLAGRDTTAGLLSFA 325
 CYP52A5B 278 PEELE-K-QSGYVFLYELVKQTRDPNVLRDQSLINILLAGRDTTAGLLSFA 325
 CYP52A8A 273 PEELE-K-QGYVFLYELVKQTRDPKVLQDQLINILLAGRDTTAGLLSFA 320
 CYP52A8B 273 PEELE-K-QGYVFLYELAKQTRDPKVLQDQLINILLAGRDTTAGLLSFA 320
 CYP52D4A 267 PEDTS----EYVFLRELVKHTRDPVVLQDQALNVLLAGRDTTAGLLSFA 311
 ***** ** ** ** ** ***** **

CYP52A1A 333 LFELARHPMWSKLRREEIVNFCVGEDSRVVEEITFEALKRCEYLKAILNE 382
 CYP52A2A 331 PFELARNPEVTNKLREEIEDKFGIGENASVEDISFESLKSCEYLKAVLNE 380
 CYP52A2B 331 PFELARNPEVTNKLREEIEDKFGIGENARVEDISFESLKSCEYLKAVLNE 380
 CYP52A3A 349 FYELSRNPEVFAKLREVENRFGIGEEARVEEISFESLKSCEYLKAVINE 398
 CYP52A3B 349 FYELSRNPEVFAKLREVENRFGIGEEARVEEISFESLKSCEYLKAVINE 398
 CYP52A5A 326 VFELARHPEIWAKLREEIEQQFGIGEDSRVVEEITFESLKRCEYLKAPLINE 375
 CYP52A5B 326 VFELARNPHIWAKLREEIEQQFGIGEDSRVVEEITFESLKRCEYLKAVINE 375
 CYP52A8A 321 VFELARNPHIWAKLREEIEQQFGIGEDSRVVEEITFESLKRCEYLKAVINE 370
 CYP52A8B 321 VFELARNPHIWAKLREEIESHFGIGEDSRVVEEITFESLKRCEYLKAVINE 370
 CYP52D4A 312 TFEELARNPHIWAKLREEIVLTGPFSSD----EITVAGLKSCEYLKAVINE 357
 . ***** *

FIG. 16B-2

CYP52A1A	383	TLRMYPSPVNFRTATRTTLPRGGGANGTDPIYIPKGSTVAVVVKTHR	432
CYP52A2A	381	TLRLYPSPQNFVRVATKNTTLPRGGKGKGLSPVLVRKQGTIVYGVAAHR	430
CYP52A2B	381	TLRLYPSPQNFVRVATKNTTLPRGGKGKGLSPVLVRKQGTIVYGVAAHR	430
CYP52A3A	399	TLRLYPSPVPHNFVRATNTTLPRGGGSDGYSPIVVRKKGQVMVTVIGTHR	448
CYP52A3B	399	ALRLYPSPVPHNFVRATNTTLPRGGGSDGYSPIVVRKKGQVMVTVIGTHR	448
CYP52A5A	376	TLRLYPSPVRNFRATKNTTLPRGGGSDGTSPILOKGEAVSYGINSTHL	425
CYP52A5B	376	TLRLYPSPVRNFRATKNTTLPRGGGSDGTSPILOKGEAVSYGINSTHL	425
CYP52A8A	371	TLRLHPSVPRNARFAIKDNTTLPRGGGPDGTPILIRKDEWVQYSISATQT	420
CYP52A8B	371	TLRLHPSVPRNARFAIKDNTTLPRGGGPDGTPILIRKDEWVQYSISATQT	420
CYP52D4A	358	TLRLYPSPVRNARFATNTTLPRGGGPDGTSFPIILIRKQDPVGYFICATHL	407
		.** * * * * *	
CYP52A1A	433	LEEVYGDANDFRPERWFEPSTKLGWAYVPFNGGPRVCLGQOFALTEAS	482
CYP52A2A	431	NPAYVGKDALEFRPERWFEPETKLGWAFLPFNGGPRICLGQOFALTEAS	480
CYP52A2B	431	NPAYVGKDALEFRPERWFEPETKLGWAFLPFNGGPRICLGQOFALTEAS	480
CYP52A3A	449	DPSYGDADVFRPERWFEPETKLGWAYVPFNGGPRICLGQOFALTEAS	498
CYP52A3B	449	DPSYGDADVFRPERWFEPETKLGWAYVPFNGGPRICLGQOFALTEAS	498
CYP52A5A	426	DPVYGGDAAEFRPERWFEPSTKLGWAYLPFNGGPRICLGQOFALTEAG	475
CYP52A5B	426	DPVYGGDAAEFRPERWFEPSTKLGWAYLPFNGGPRICLGQOFALTEAG	475
CYP52A8A	421	NPAYYGADAADFRPERWFEPSTRLNGWAFLPFNGGPRICLGQOFALTEAG	470
CYP52A8B	421	NPAYYGADAADFRPERWFEPSTRLNGWAFLPFNGGPRICLGQOFALTEAG	470
CYP52D4A	408	NEKYVNDSHVFRPERWAALEKSLGWSYLPFNGGPRICLGQOFALILEAS	457
		.** * * * * *	

FIG. 16C-I

CYP52A1A	483	YVITRLAQMPETVSSDPGLEYPKPKCIHLTMSHNDGVFKM	523
CYP52A2A	481	YVTVRLLOEFAHLSMDPDTEYPPKMSHLTMSLFDGANIEM	522
CYP52A2B	481	YVTVRLLOEFGHLSMDPNTTEYPPKMSHLTMSLFDGANIEM	522
CYP52A3A	499	YVTVRLLOEFAHLSMDPDTEYPPKLQNTLTLSLFDGADVRY	540
CYP52A3B	499	YVTVRLLOEFGNLSLDPNAEYPPKLQNTLTLSLFDGADVRF	540
CYP52A5A	476	YVLVRLVQEFSHVRLDPDEVYPPKRLTNLTMCLODGAIVKFD	517
CYP52A5B	476	YVLVRLVQEFSHRLDPDEVYPPKRLTNLTMCLODGAIVKFD	517
CYP52A8A	471	YVLVRLVQEFPSLSQDPETKYPPPLAHLTMCLFDGAHVKMS	512
CYP52A8B	471	YVLVRLVQEFPSLSQDPETKYPPPLAHLTMCLFDGAHVKMQ	512
CYP52D4A	458	YVLARLTQCYYTTIQLR-TTEYPPKLVHLTMSLLNGVYIRTRT	499
		** *	

FIG. 16C-2

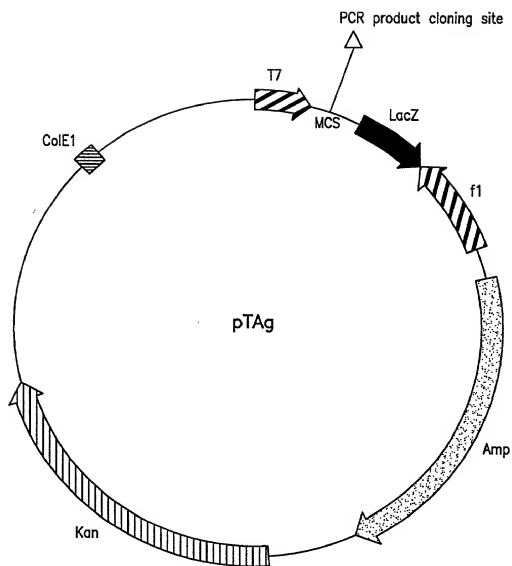


FIG. 17

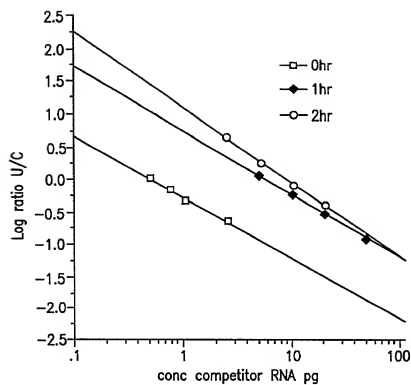


FIG. 18

Applicants: C. Wilson, et al.

Filing Date: Herewith

Serial No.: To be assigned (Div. of Ser. No.09/302,620)

Title: CYTOCHROME P450 MONOOXYGENASE

Docket: 1010-16DIV

Sheet 70 of 89

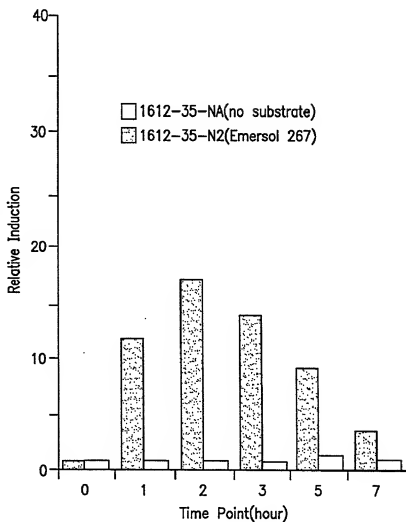


FIG. 19

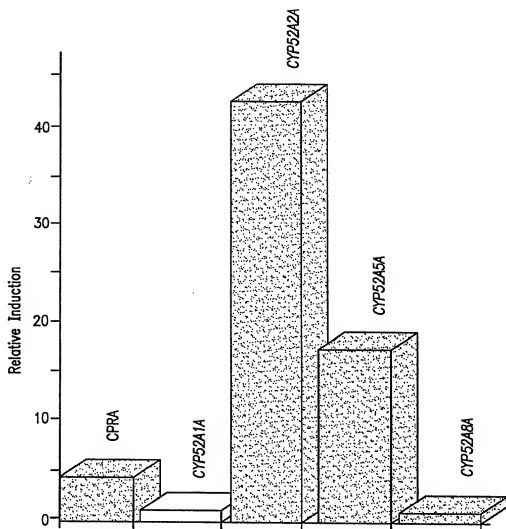


FIG. 20

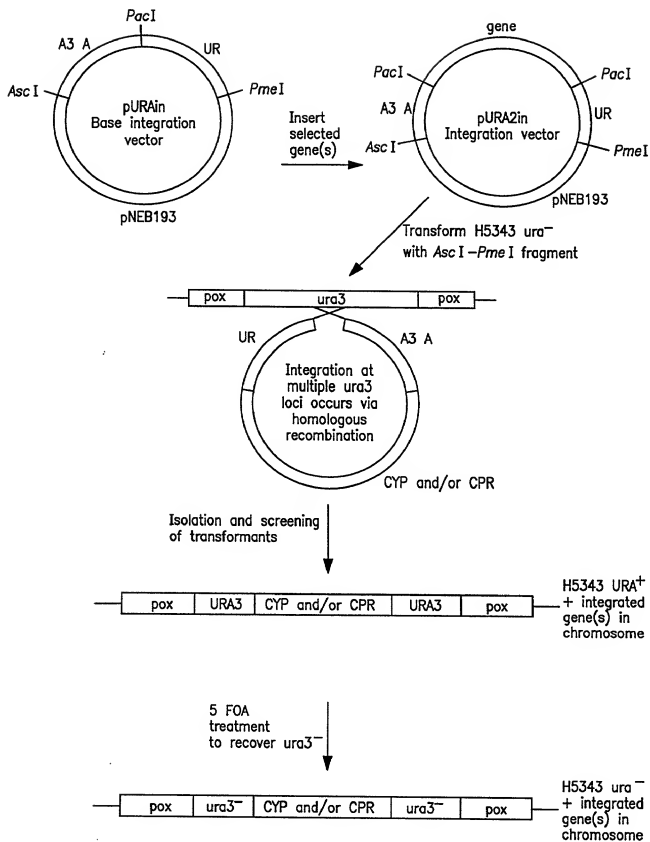


FIG. 2I

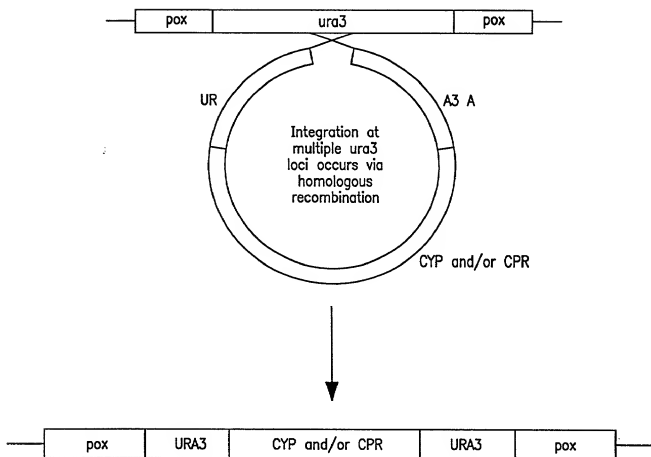


FIG. 22

Sequence Range: 1 to 1712

10	20	30	40	50	60	70	80
GGTACCGAGC	TCACAGATT	TGGGATTTTC	GAGTTTGGAT	TGTTTCCTTT	GTTGATTGAA	TTGACGAAAC	CAGAGGTTTT
90	100	110	120	130	140	150	160
CAAGACAGAT	AAGATTGGGT	TTATCAAAAC	GCAGTTTGA	ATATTCAGT	TGCTTTCCAA	GATATCTTGA	AGAAGATTGA
170	180	190	200	210	220	230	240
CGATTTGAAA	TTTGAGAAG	TGGAGAAGAT	CTGGTTTGA	TTGTTGGAGA	ATTTCAGAA	TCTCAAGATT	TACTCTAACG
250	260	270	280	290	300	310	320
ACGGGTACAA	CGAGAATTGT	ATTGAATTGA	TCAGAAGACAT	GATCTTGGTG	TTACAGAACA	TCAAGTTCTT	GGACCAGACT
330	340	350	360	370	380	390	400
GAGAAATGCCA	CAGATATACA	AGCGGTCAATG	TGATAAAATG	GATGAGATTT	ATCCCACAAT	TGAAGAAAGA	GTTTATGGAA
410	420	430	440	450	460	470	480
AGTGGTCAAC	CAGAAGCTAA	ACAGGAGAA	GCAAAACGAG	AGGTGAACA	AGAAGAAGAA	GGTAAATAAG	TATTTTGTAT
490	500	510	520	530	540	550	560
TATATAACA	ACAAAGTAAG	GAATACAGAT	TTATACAATA	AATTGCCATA	CTAGTCACGT	GAGATATCTC	ATCCATTCCC
570	580	590	600	610	620	630	640
CBACTCCCAA	GAATAAATAA	AAGTGAAAAA	AAAAATCAAA	CCCAAGATC	AACCTCCCCA	TCATCATCGT	CATCAAAACC

FIG. 23A

650	CCAGCTCAAT	TCGCAATGGT	TAGCACAATA	ACATACACAG	AAAGGGCATC	AGCACACCCC	TCCAGAGTTG	CCCAACGTTT
		M V S I K	T Y T	E R A S	A H P	S K V	A Q R	L>
730	ATTCGGTTA	ATGAGTCCA	AAAAGACCAA	CCTCTGGCC	TCGATCGAG	TGACCACNAAC	CGCCGAGTTC	CTTTGCTCA
	F R L	M E S	K K T N	L C A S	I D V	T T T A	E F L S	L>
810	TCGACAAGCT	CGGTCCCCAC	ATCTGCTCG	TGAAGACGCA	CATCGATATC	ATCTCAGACT	TCAGCTACGA	GGGCACGATT
	I D K L	G P H	I C L	V K T H	I D I	I S D F	S Y E G	T I>
890	GAGCCGTTGC	TTGTGCTTGC	AGAGCGCCAC	GGGTTCTTGA	TATTCGAGGA	CAGGAAGTTT	GCTGATATCG	GAACACCCGT
	E P L	L V L A	E R H	G F L	I F E D	R K F A	D I G N	T V>
970	GATGTTGAG	TACACCTCGG	GGGTATACCG	GATCGCGCG	TGGAGTGACA	TCACGAACGC	GCACGGAGTG	ACTGGGAAGG
	M L Q	Y T S	G V Y R	I A A W	S D I	T N A H	G V T G	K>
1050	CGGTGCTTGA	AGGGTTGAAA	CGCGGTGCGG	AGGGGTAGA	AAAGGAAGG	GGCGTGTGA	TGTTGGCGGA	GTTGTCGAGT
	G V V E	G L K	R G A	E G V E	K E R G	V L M L	A E L S	S>
1130	AAAGGCTCGT	TGGCGCATGG	TGAATATACC	CGTGAGACGA	TCGAGATTGC	GAAGAGTGAT	CGGGAGTTCG	TGATTGGGTT
	K G S	L A H G	E Y T	R E T	I E I A	K S D R	E F V I	G F>

FIG. 23B

1210	1220	1230	1240	1250	1260	1270	1280
CATCGCCAG	CGGACATGG	GGGATAGAGA	AGAAGGGTTT	GATTGGATCA	TCATGACGCC	TGGTGTGGGG	TTGGATGATA
I A Q	R D M	G G R E	E G F	D W I	I M T P	G V G	L D D>
1290	1300	1310	1320	1330	1340	1350	1360
AAGCGATGC	GTTCGGCCAG	CAGTATAGGA	CTCTTTCATGA	GGTGGTTCCTG	ACTGGTACCG	ATGTGATTAT	TGTCGGGAGA
K G D A	L G Q	Q Y R	T V D E	V V L	T G T	D V I	I V G R>
1370	1380	1390	1400	1410	1420	1430	1440
GGGTTGTTG	GAAAAGGAAG	AGACCTGAG	GTGGAGGGAA	AGAGATACAG	GGATGCTGGA	TGGAAGGCAT	ACTTGAAGAG
G L F	G K G R	D P E	V E G	K R Y R	D A G	W K A	Y L K R>
1450	1460	1470	1480	1490	1500	1510	1520
AACTGGTCAG	TTAGAAATAAA	TATTGTAATA	AATAGGTCTA	TATACATACA	CTAAGCTTCT	AGGACGTCAT	TGTAGTCTTC
T G Q	L E *	>					
1530	1540	1550	1560	1570	1580	1590	1600
GAAGTTGTCT	GCTAGTTTAG	TTCTCATGAT	TTTCGAAAACC	AATACGCAA	TGGATGTAGC	AGGGATGGTG	GTTAGTGCCT
1610	1620	1630	1640	1650	1660	1670	1680
TCCTTGACAA	CCCAGAGTAC	GCCGCCCTCAA	ACCACGTAC	ATTGCGCCTT	TGCTTTCATCC	GCATCACTTG	CTTGAAGSTA
1690	1700	1710					
TCCACGTACG	AGTTGTAATA	CACCTTGAAG	AA				

FIG. 23C

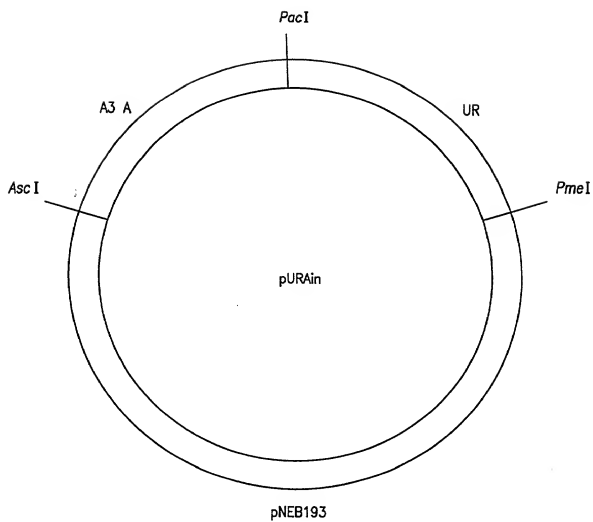


FIG. 24

A circular plasmid vector map. The plasmid is represented by a circle. A shaded arc on the right side contains multiple restriction enzyme sites, labeled from top to bottom: EcoRI, SacI, KpnI, SmaI, BamHI, AscI, PacI, SalI, PmeI, AatI, PstI, SphI, and HindIII. A larger shaded arc on the left is labeled 'Amp^r'. A small arrowhead on the right is labeled 'lac Z[']'. A diamond-shaped element at the bottom is labeled 'ORI'.

FIG. 25

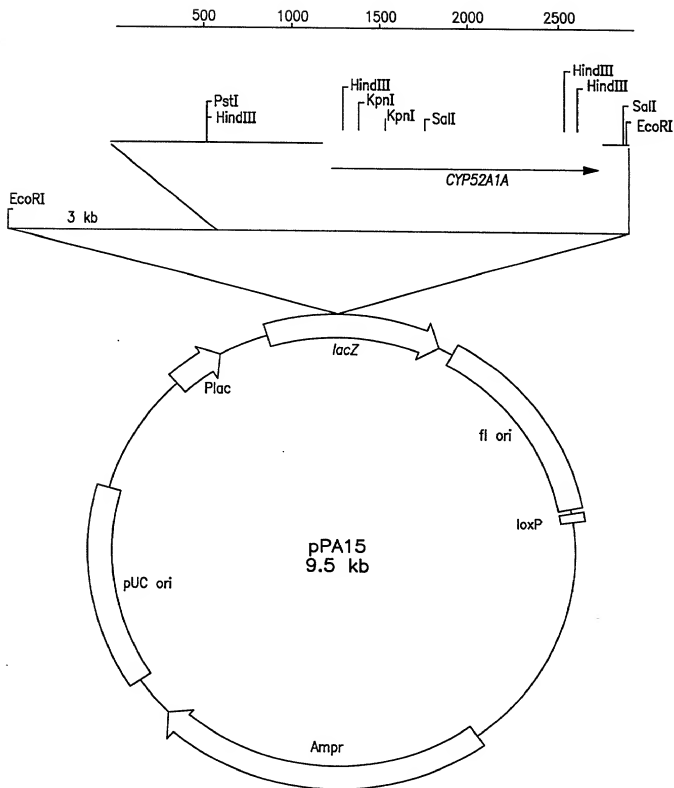


FIG. 26

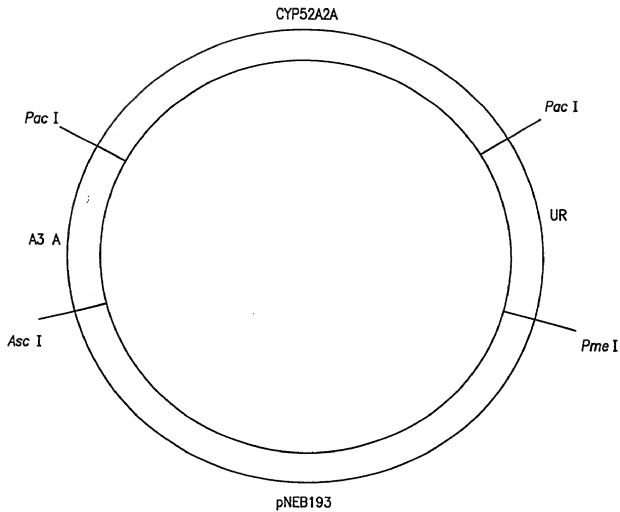


FIG. 27

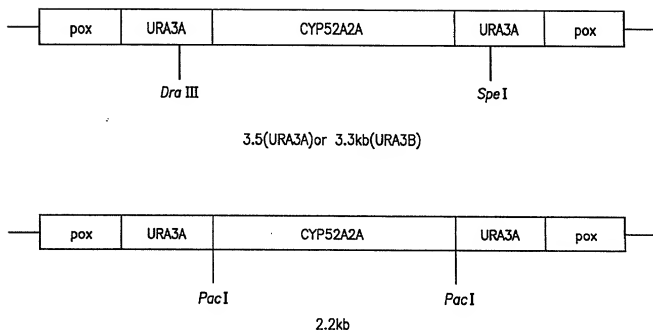


FIG. 28

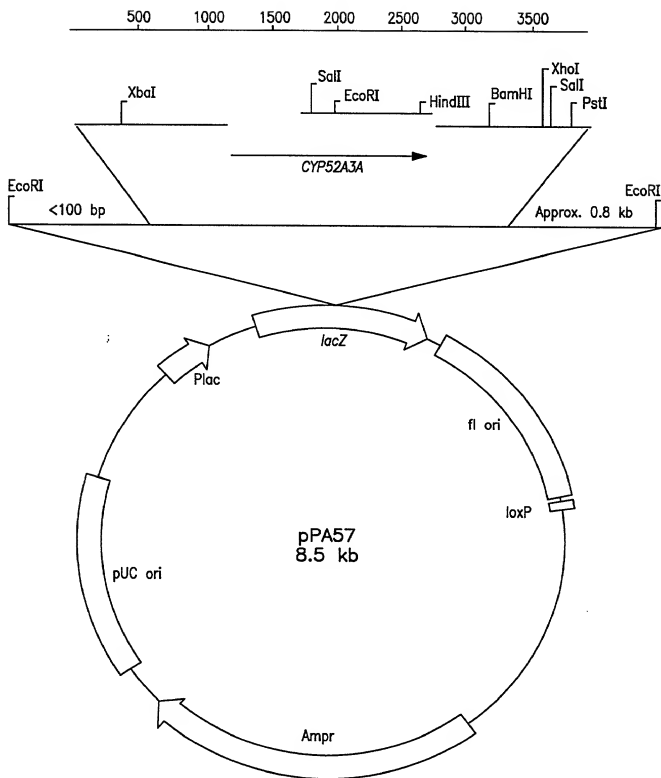


FIG. 29

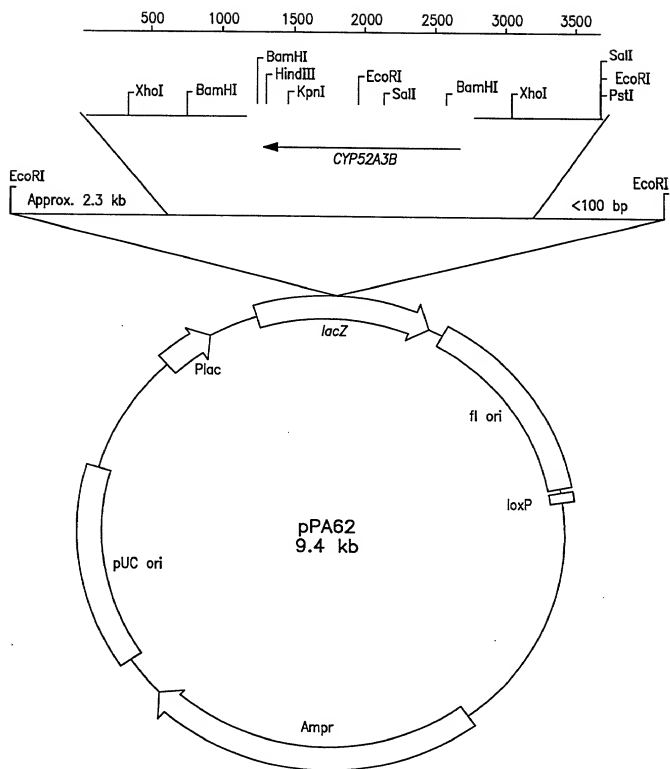


FIG. 30

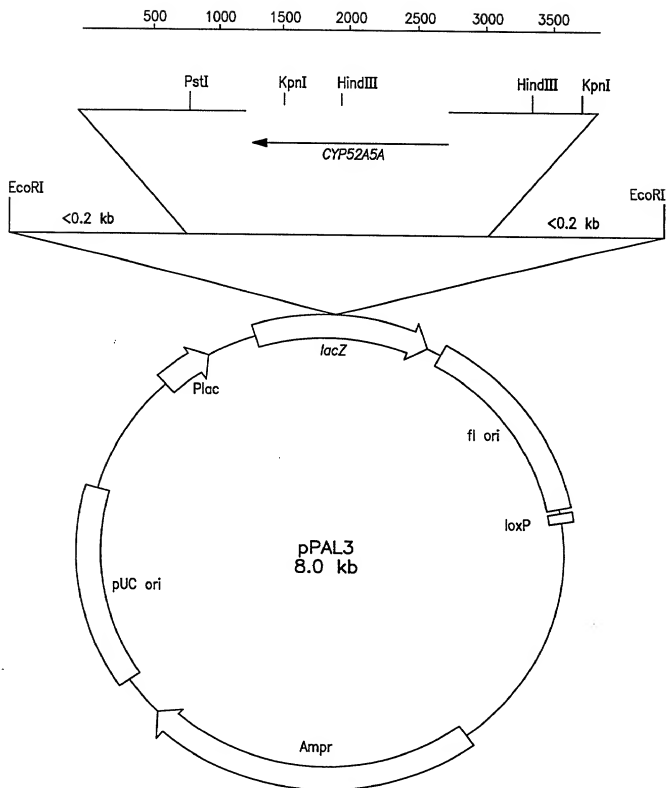


FIG. 31

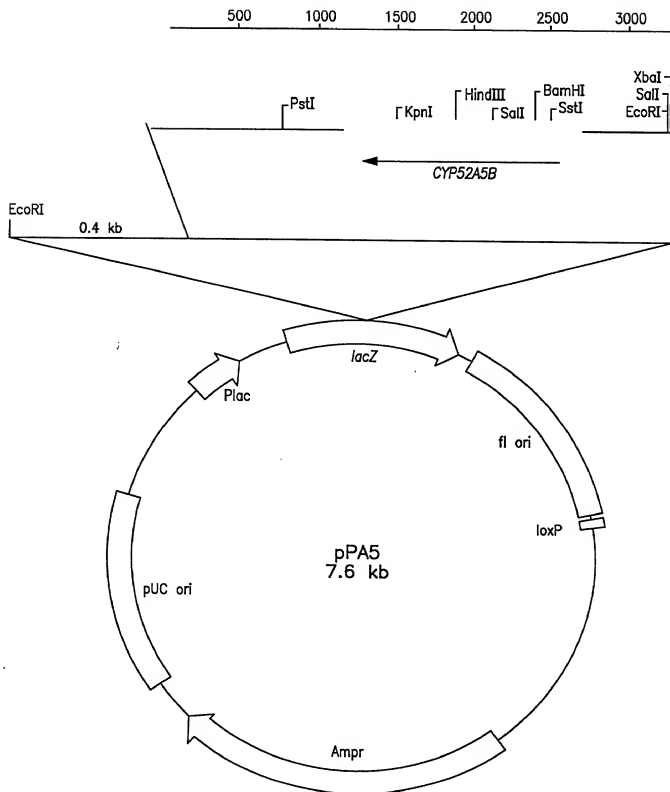


FIG. 32

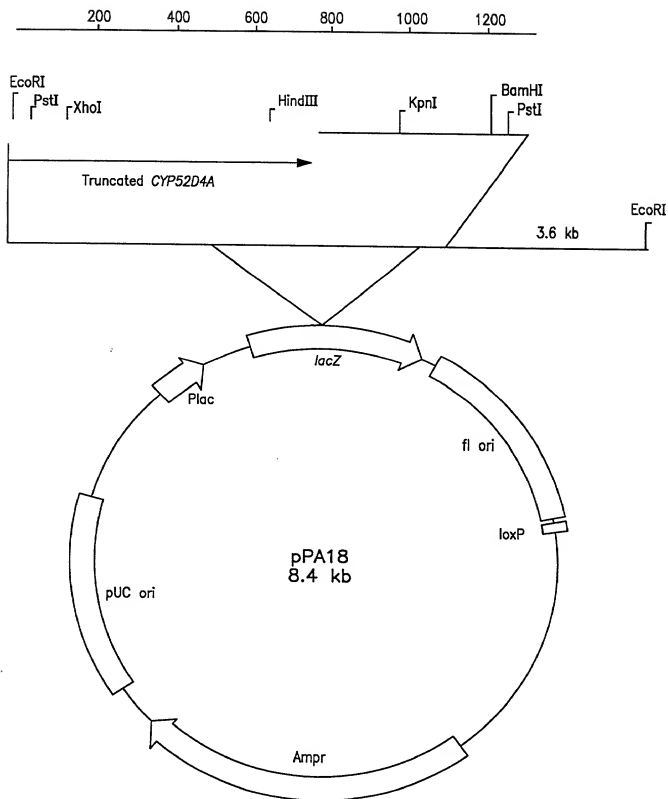


FIG. 33

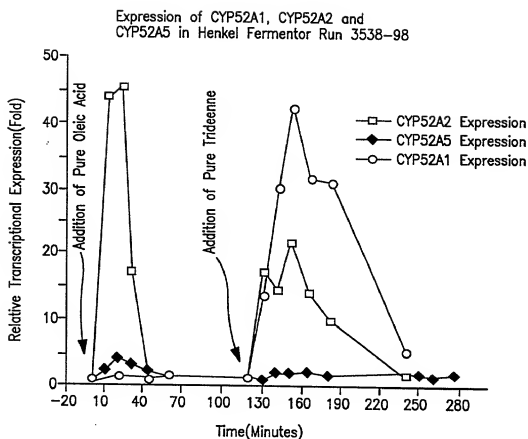
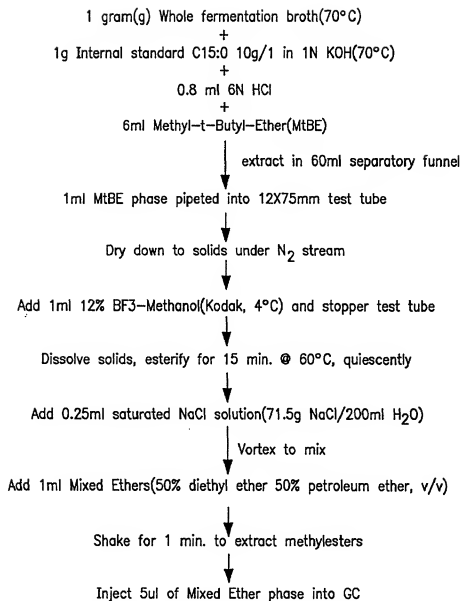


FIG. 34



GC parameters

Column : HP-INNOWAX capillary column, 30m X 0.32mm, 0.5 μ m film thickness

Split Ratio : 1:100

Column Head Pressure : 13.5 psig

Injector Temperature : 240°C

FID Detector Temp. : 250°C

Temp. Prog. : 90°C for 0 min. to 190°C @ 7°C/min. for 0 min. to 235°C @ 12°C/min. for 30 min.

FIG. 35

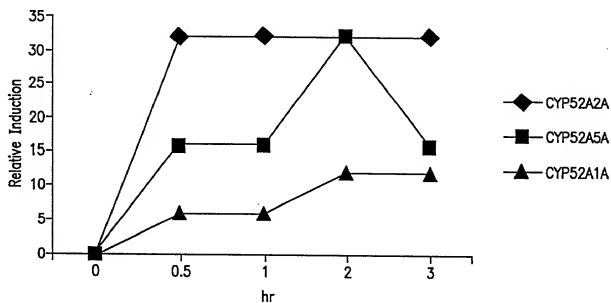


FIG. 36